

SUBSTITUTE SEQUENCE LISTING

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 Bougueleret Lydie

<120> Extended cDNAs

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<140> 09/215,435

<141> 1998-12-17

<150> 60/069,957

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<150> 60/074,121

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 agggaggagg aaacagcgtg agtcc 25

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 agcagcaaca atcaggacag cacag 25

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atcaagaatt cgcacgagac catta

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<211> 67

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<222> 67

<223> n=a, g, c or t

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ttttttn

60

67

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<213> Artificial Sequence

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ccagcagagt cacgagagag actacacgg

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cacgagagag actacacggt actgg

25

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<213> Homo Sapiens

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 <222> 90..140
 <223> Von Heijne matrix

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 <222> 290
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 aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca 60
 gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc 113
 Met Lys Lys Val Leu Leu Leu Ile
 -15 -10
 aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag 161
 Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
 -5 1 5
 gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr 209
 Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
 10 15 20
 wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att 257
 Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
 25 30 35
 cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata 305
 Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
 40 45 50 55
 cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
 Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
 60 65
 ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat 414
 caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
 gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa 526

<210> 18
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 <212> PRT
 <213> Homo Sapiens

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 <222> 1..17

<223> Von Heijne matrix
score 8.2
seq LLLITAILAVAVG/FP

<400> 18
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

<210> 19
<211> 822
<212> DNA
<213> Homo Sapiens

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<222> 118..184
<223> blastn

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<222> 56..113
<223> blastn

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<222> 454..485
<223> blastn

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<223> blastn

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<222> 65..369
<223> blastn

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<222> 61..399
<223> blastn

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<222> 408..458
<223> blastn

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<222> 60..399

<223> blastn

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<221> misc_feature

<222> 393..432

<223> blastn

<220>

<221> sig_peptide

<222> 346..408

<223> Von Heijne matrix

<220>

<221> misc_feature

<222> 115

<223> n=a, g, c or t

<400> 19

actcctttta	gcataggggc	ttcggcgcca	gcggccagcg	ctagtcggtc	tggttaagtgc	60
ctgatgccga	gttcggtctc	tcggtctctt	tcctgggtccc	aggcaaagcg	gasgnagatc	120
ctcaaacggc	ctagtgtctc	gcgcttcggy	agaaaatcag	cggtctaatt	aattcctctg	180
gtttgttgaa	gcagttacca	agaatcttca	accctttccc	acaaaagcta	attgagtaca	240
cgttcctgtt	gagtacacgt	tcctgttgat	ttacaaaagg	tcaggtatg	agcaggtctg	300
aagactaaca	ttttgtgaag	ttgtaaaaca	gaaaacctgt	tagaa atg	tgg tgg ttt	357
				Met Trp Trp Phe		
				-20		

cag	caa	ggc	ctc	agt	ttc	ctt	cct	tca	gcc	ctt	gta	att	tgg	aca	tct	405
Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val	Ile	Trp	Thr	Ser	
	-15						-10				-5					

gct	gct	ttc	ata	ttt	tca	tac	att	act	gca	gta	aca	ctc	cac	cat	ata	453
Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	Leu	His	His	Ile	
	1			5					10					15		

gac	ccg	gct	tta	cct	tat	atc	agt	gac	act	ggt	aca	gta	gct	cca	raa	501
Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	Val	Ala	Pro	Xaa	
			20					25				30				

aaa	tgc	tta	ttt	ggg	gca	atg	cta	aat	att	gcg	gca	gtt	tta	tgt	caa	549
Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys	Gln	
		35					40					45				

aaa	tagaaatcag	gaarataatt	caacttaaag	aakttcattt	catgaccaa	602
Lys						

ctcttcaraa	acatgtcttt	acaagcatat	ctcttgatt	gctttctaca	ctgttgaatt	662
gtctggcaat	atttctgcag	tggaaaattt	gatttarmta	gttcttgact	gataaatatg	722
gtaagggtggg	cttttcccc	tgtgtaattg	gctactatgt	cttactgagc	caagttgtaw	782
tttgaaataa	aatgatatga	gagtgcacaca	aaaaaaaaaa			822

<210> 20

<211> 21

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> 1..21

<223> Von Heijne matrix

score 5.5

seq SFLPSALVIWTS/AF

<400> 20

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
1 5 10 15
Ile Trp Thr Ser Ala
20

<210> 21

<211> 405

<212> DNA

<213> Homo Sapiens

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<222> complement(103..398)

<223> blastn

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<222> 185..295

<223> Von Heijne matrix

<400> 21

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cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggccctacct 120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
-35 -30 -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
-20 -15 -10
ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg 325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
-5 1 5 10
cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc 374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaaa a 405

<210> 22

<211> 37

<212> PRT

<213> Homo Sapiens

<220>

<221> SIGNAL

<222> 1..37

<223> Von Heijne matrix

score 5.9

seq LSYASSALSPCLT/AP

<400> 22

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1 5 10 15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
20 25 30
Ser Pro Cys Leu Thr
35

<210> 23
 <211> 496
 <212> DNA
 <213> Homo Sapiens

<220>
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 <222> 149..331
 <223> blastn

<220>
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 <222> 328..485
 <223> blastn

<220>
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 <223> blastn

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 <222> 196..240
 <223> Von Heijne matrix

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 <222> 101
 <223> n=a, g, c or t

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 attagccgtg gcctaggccg tttaacgggg tgacacgagc ntgcagggcc gagtccaagg 120
 cccggagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag 180
 gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt 231
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
 -15 -10 -5
 gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt 279
 Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
 1 5 10
 gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg 327
 Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
 15 20 25
 gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat 375
 Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
 30 35 40 45
 tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc 424
 Ser Ser Ala
 atatttaaatt tggaaaagtc aaattgasca ttattaaata aagcttgttt aatatgtctc 484
 aaacaaaaaa aa 496

<210> 24
 <211> 15
 <212> PRT
 <213> Homo Sapiens

<220>
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 <222> 1..15
 <223> Von Heijne matrix
 score 5.5
 seq ILSTVTALTTFAXA/LD

<220>
 <221> UNSURE
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 <223> Xaa = any one of the twenty amino acids

<400> 24
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
 1 5 10 15

<210> 25
 <211> 623
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix

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 aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg 57
 Met Glu Arg
 -15
 ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
 Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
 -10 -5 1
 tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
 Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
 5 10 15
 gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
 Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
 20 25 30 35
 caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta 249
 Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
 40 45 50
 cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac 297
 Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
 55 60 65
 atg aak ttc gaa tgg tgc ccg gcc ccc atg gtg caa gcc gtg atc acc 345
 Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
 70 75 80
 agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag 393
 Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
 85 90 95
 gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tgc 441
 Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
 100 105 110 115
 agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc 489
 Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
 120 125 130

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ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
      135              140              145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa      594
taaactctca tgcccccaaa aaaaaaaaaa      623

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<210> 26
<211> 16
<212> PRT
<213> Homo Sapiens

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<220>
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<222> 1..16
<223> Von Heijne matrix
      score 10.1
      seq LVLTLCTLPLAVA/SA

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<400> 26
Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
1              5              10              15

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<210> 27
<211> 848
<212> DNA
<213> Homo Sapiens

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<222> 32..73
<223> Von Heijne matrix

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<400> 27
aactttgcct tgtgttttcc accctgaaag a atg ttg tgg ctg ctc ttt ttt      52
                        Met Leu Trp Leu Leu Phe Phe
                        -10
ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat      100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
      -5              1              5
gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca      148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
10              15              20              25
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct      196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
      30              35              40
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat      244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
      45              50              55
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt      292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
      60              65              70
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca      340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
      75              80              85
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat      388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Ala Phe Phe Leu Asn
90              95              100              105

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gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc	436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro	
110 115 120	
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt	484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe	
125 130 135	
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg	532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp	
140 145 150	
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa	580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu	
155 160 165	
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat	628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp	
170 175 180 185	
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag	676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu	
190 195 200	
gat gag agg ctc acc cct ctc tgaagggctg ttgttctgct tcctcaaraa	727
Asp Glu Arg Leu Thr Pro Leu	
205	
attaaacatt tgtttctgtg tgactgctga gcattcctgaa ataccaagag cagatcatat	787
wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa	847
c	848

<210> 28
 <211> 14
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> SIGNAL
 <222> 1..14
 <223> Von Heijne matrix
 score 10.7
 seq LWLLFFLVTAIHA/EL

<400> 28
 Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
 1 5 10

<210> 29
 <211> 25
 <212> DNA
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<220>
 <223> oligonucleotide

<400> 29
 gggaagatgg agatagtatt gcctg 25

<210> 30
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 30
ctgccatgta catgatagag agattc

26

<210> 31
<211> 546
<212> DNA
<213> Homo Sapiens

<220>
<221> promoter
<222> 1..517

<220>
<223> codon_start="518"

<220>
<221> protein_bind
<222> 17..25
<223> matinspector prediction
name CMYB_01
score 0.983
sequence tgtcagttg

<220>
<221> protein_bind
<222> complement(18..27)
<223> matinspector prediction
name MYOD_Q6
score 0.961
sequence cccaactgac

<220>
<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

<220>
<221> protein_bind
<222> 94..104
<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag

<220>
<221> protein_bind
<222> complement(129..139)
<223> matinspector prediction
name DELTAEF1_01
score 0.960
sequence gcacacctcag

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<220>
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<222> complement(155..165)
<223> matinspector prediction
      name GATA_C
      score 0.964
      sequence agataaatcca

<220>
<221> protein_bind
<222> 170..178
<223> matinspector prediction
      name CMYB_01
      score 0.958
      sequence cttcagttg

<220>
<221> protein_bind
<222> 176..189
<223> matinspector prediction
      name GATA1_02
      score 0.959
      sequence ttgtagataggaca

<220>
<221> protein_bind
<222> 180..190
<223> matinspector prediction
      name GATA_C
      score 0.953
      sequence agataggacat

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<221> protein_bind
<222> 284..299
<223> matinspector prediction
      name TAL1ALPHA47_01
      score 0.973
      sequence cataacagatggtaag

<220>
<221> protein_bind
<222> 284..299
<223> matinspector prediction
      name TAL1BETA47_01
      score 0.983
      sequence cataacagatggtaag

<220>
<221> protein_bind
<222> 284..299
<223> matinspector prediction
      name TAL1BETA1TF2_01
      score 0.978
      sequence cataacagatggtaag

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<220>
<221> protein_bind
<222> complement(287..296)
<223> matinspector prediction
      name MYOD_Q6
      score 0.954
      sequence accatctggt

<220>
<221> protein_bind
<222> complement(302..314)
<223> matinspector prediction
      name GATA1_04
      score 0.953
      sequence tcaagataaagta

<220>
<221> protein_bind
<222> 393..405
<223> matinspector prediction
      name IK1_01
      score 0.963
      sequence agttgggaattcc

<220>
<221> protein_bind
<222> 393..404
<223> matinspector prediction
      name IK2_01
      score 0.985
      sequence agttgggaattc

<220>
<221> protein_bind
<222> 396..405
<223> matinspector prediction
      name CREL_01
      score 0.962
      sequence tgggaattcc

<220>
<221> protein_bind
<222> 423..436
<223> matinspector prediction
      name GATA1_02
      score 0.950
      sequence tcagtgatatggca

<220>
<221> protein_bind
<222> complement(478..489)
<223> matinspector prediction
      name SRY_02
      score 0.951
      sequence taaaacaaaaca

<220>

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<221> protein_bind
 <222> 486..493
 <223> matinspector prediction
 name E2F_02
 score 0.957
 sequence tttagcgc

<220>
 <221> protein_bind
 <222> complement(514..521)
 <223> matinspector prediction
 name MZF1_01
 score 0.975
 sequence tgagggga

<400> 31
 tgagtgcagt gttacatgtc agttgggtta agtttggtta tgtcattcaa atcttctatg 60
 tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat ggttctatta 120
 gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
 gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
 atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300
 atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta 360
 gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
 catcagtgat atggcaaagc tgggactaag ggtagtgatc agagggttaa aattgtgtgt 480
 tttgttttag cgctgctggg gcatcgccct gggccccctc aaacagattc ccatgaatct 540
 cttcat 546

<210> 32
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 32
 gtaccaggga ctgtgacat tgc 23

<210> 33
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 33
 ctgtgacat tgctcccaag agag 24

<210> 34
 <211> 861
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> promoter
 <222> 1..806

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<220>
<223> codon_start="807"

<220>
<221> protein_bind
<222> complement(60..70)
<223> matinspector prediction
      name NFY_Q6
      score 0.956
      sequence ggaccaatcat

<220>
<221> protein_bind
<222> 70..77
<223> matinspector prediction
      name MZF1_01
      score 0.962
      sequence cctgggga

<220>
<221> protein_bind
<222> 124..132
<223> matinspector prediction
      name CMYB_01
      score 0.994
      sequence tgaccgttg

<220>
<221> protein_bind
<222> complement(126..134)
<223> matinspector prediction
      name VMYB_02
      score 0.985
      sequence tccaacggt

<220>
<221> protein_bind
<222> 135..143
<223> matinspector prediction
      name STAT_01
      score 0.968
      sequence ttcctggaa

<220>
<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
      name STAT_01
      score 0.951
      sequence ttccaggaa

<220>
<221> protein_bind
<222> complement(252..259)
<223> matinspector prediction
      name MZF1_01

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score 0.956
sequence ttggggga

<220>

<221> protein_bind

<222> 357..368

<223> matinspector prediction

name IK2_01

score 0.965

sequence gaatgggatttc

<220>

<221> protein_bind

<222> 384..391

<223> matinspector prediction

name MZF1_01

score 0.986

sequence agagggga

<220>

<221> protein_bind

<222> complement(410..421)

<223> matinspector prediction

name SRY_02

score 0.955

sequence gaaaacaaaaca

<220>

<221> protein_bind

<222> 592..599

<223> matinspector prediction

name MZF1_01

score 0.960

sequence gaagggga

<220>

<221> protein_bind

<222> 618..627

<223> matinspector prediction

name MYOD_Q6

score 0.981

sequence agcatctgcc

<220>

<221> protein_bind

<222> 632..642

<223> matinspector prediction

name DELTAEF1_01

score 0.958

sequence tcccaccttcc

<220>

<221> protein_bind

<222> complement(813..823)

<223> matinspector prediction

name S8_01

score 0.992

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sequence gaggcaattat

<220>
<221> protein_bind
<222> complement(824..831)
<223> matinspector prediction
      name MZF1_01
      score 0.986
      sequence agagggga

<220>
<221> misc_feature
<222> 335,376
<223> n=a, g, c or t

<400> 34
tactataggg cacgcgtggt cgacggccgg gctgttctgg agcagagggc atgtcagtaa      60
tgattgggtcc ctggggaagg tctggctggc tccagcacag tgaggcattt aggtatctct      120
cgggtgaccgt tggattcctg gaagcagtag ctgttctggt tggatctggt agggacaggg      180
ctcagagggc taggcacgag ggaaggtcag aggagaaggs aggsarggcc cagtgagarg      240
ggagcatgcc ttccccaac cctggcttsc ycttggyam agggcgkty tgggmacttr      300
aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcaca tagcctgaat      360
gggatttcag gttagncagg gtgagagggg aggcctctct gcttagtttt gttttgtttt      420
ccaaatcaag gtaacttgct cccttctgct acgggccttg gtcttggtt gtctctaccc      480
agtcggaact ccctaccact ttcaggagag tggttttagg cccgtggggc tgttctgttc      540
caagcagtggt gagaacatgg ctggtagagg ctctagctgt gtgcgggggc tgaaggggag      600
tgggttctcg cccaaagagc atctgcccac ttcccacctt cccttctccc accagaagct      660
tgcttgagct gtttgacaaa aaatccaaac cccacttggc tactctggcc tggcttcage      720
ttggaacca atacctaggg ttacaggcca tcttgagcca ggggcctctg gaaattctct      780
tcttgatggt cttttaggtt tgggcacaaa atataattgc ctctccctc tcccattttc      840
tctcttgga gcaatggtca c                                     861

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 35
ctgggatgga aggcacggta                                     20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 36
gagaccacac agctagacaa                                     20

<210> 37
<211> 555
<212> DNA

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<213> Homo Sapiens

<220>
<221> promoter
<222> 1..500

<220>
<223> codon_start="501"

<220>
<221> protein_bind
<222> 191..206
<223> matinspector prediction
      name ARNT_01
      score 0.964
      sequence ggactcacgtgctgct

<220>
<221> protein_bind
<222> 193..204
<223> matinspector prediction
      name NMYC_01
      score 0.965
      sequence actcacgtgctg

<220>
<221> protein_bind
<222> 193..204
<223> matinspector prediction
      name USF_01
      score 0.985
      sequence actcacgtgctg

<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name USF_01
      score 0.985
      sequence cagcacgtgagt

<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name NMYC_01
      score 0.956
      sequence cagcacgtgagt

<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name MYCMAX_02
      score 0.972
      sequence cagcacgtgagt

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<220>
<221> protein_bind
<222> 195..202
<223> matinspector prediction
name USF_C
score 0.997
sequence tcacgtgc

<220>
<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
name USF_C
score 0.991
sequence gcacgtga

<220>
<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga

<220>
<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct

<220>
<221> protein_bind
<222> 400..409
<223> matinspector prediction
name CETS1P54_01
score 0.974
sequence tccggaagcc

<220>
<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1_Q4
score 0.963
sequence agtgactgaac

<220>
<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac

<220>

<221> protein_bind
 <222> 547..555
 <223> matinspector prediction
 name PADS_C
 score 1.000
 sequence tgtggtctc

<400> 37
 ctatagggca cgcktgggtcg acggcccggg ctggtctggt ctgtkgtgga gtcggggtga 60
 aggacagcat ttgtkacatc tgggtctactg caccttccct ctgccgtgca cttggccttt 120
 kawaagctca gcaccggtgc ccatcacagg gccggcagca cacacatccc attactcaga 180
 aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta 240
 gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatacc aagtgattgt 300
 cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag 360
 gttgctctgc ccatgggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc 420
 cgtgtcttct gcctgtctcc gctcacatcc cacacttggtg ttcagtcact gagttacaga 480
 ttttgctctc tcaatttctc ttgtcttagt cccatcctct gttccccctgg ccagtttgtc 540
 tagctgtgtg gtctc 555

<210> 38
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 38
 ggccatacac ttgagtgc 19

<210> 39
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 39
 atatagacaa acgcacacc 19

<210> 40
 <211> 568
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..471

<220>
 <221> sig_peptide
 <222> 7..99
 <223> Von Heijne matrix
 score 6.9
 seq LLLVPSALSLLLA/LL

<220>
 <221> polyA_signal
 <222> 537..542

<220>
 <221> polyA_site
 <222> 554..568

<400> 40
 gggacc atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct 48
 Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro
 -30 -25 -20
 ctg tcg aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc 96
 Leu Ser Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu
 -15 -10 -5
 gcc ctc ctc ctg cct cac tgc cag aag ccc ttt gtg tat gac ctt cac 144
 Ala Leu Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His
 1 5 10 15
 gca gtc aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata 192
 Ala Val Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile
 20 25 30
 att tgc ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat 240
 Ile Cys Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr
 35 40 45
 aat ttt agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc 288
 Asn Phe Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser
 50 55 60
 ttt ttg ctg ggt acc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc 336
 Phe Leu Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu
 65 70 75
 att gaa gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg 384
 Ile Glu Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu
 80 85 90 95
 cct tct gga tta atc ttt tgt tgt gct ttt tgc tct gag act aaa ctc 432
 Pro Ser Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu
 100 105 110
 ttc tta tca aga caa gct atg gca gag aac ttt tcc atc taataaattt 481
 Phe Leu Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
 115 120
 aagagtagat tcattgttat ggttgagagt aggctctgac tatgtatatg tgtataataa 541
 acctacatat ccaaaaaaaaa aaaaaaa 568

<210> 41
 <211> 569
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 168..332

<220>
 <221> polyA_signal
 <222> 557..562

<400> 41
 agggggcgtg gggccatggt ggtcttgctg gcggggaaga agacctttct cccccctctc 60

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tgccgcgcct tcgcctgccg cggctgtcaa ctgcgtccgg agcgcggcgc cgagcgcagg 120
gatacggcgc ccagcggggt cagaaagcaa cattgaatgc agaagaa atg gcg gac 176
                                     Met Ala Asp
                                     1
ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cgc atg tat tat 224
Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg Met Tyr Tyr
      5              10              15
aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg gga 272
Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly
20              25              30              35
aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa aag 320
Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys
              40              45              50
aag agg agc aac taggagtcca ctctgaccca gccagagtcc aggtttccac 372
Lys Arg Ser Asn
              55
aggaagcaga tggagctcct ttcacagggg ctctgagaaa aactggagcc gatctcaaga 432
agccccacat ctctctaagg ggccccatgg cctgtttggg ggcagggtag gtcttggggc 492
actgtggggc gcctgcctgc tgatgtgggc tctaggccag cttgttgtca cgtacgtggt 552
gtgaaataaa gcccaag 569

<210> 42
<211> 895
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..251

<220>
<221> sig_peptide
<222> 51..110
<223> Von Heijne matrix
      score 5.3
      seq ALIFGGFISLIGA/AF

<220>
<221> polyA_signal
<222> 849..854

<220>
<221> polyA_site
<222> 882..895

<400> 42
ccgagagtgc cgggcggtcg gcgggtcagg gcagcccggg gcctgacgcc atg tcc 56
                                     Met Ser
                                     -20
cgg aac ctg cgc acc gcg ctc att ttc ggc ggc ttc atc tcc ctg atc 104
Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile
      -15              -10              -5
ggc gcc gcc ttc tat ccc atc tac ttc cgg ccc cta atg aga ttg gag 152
Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg Leu Glu
      1              5              10
gag tac aag aag gaa caa gct ata aat cgg gct gga att gtt caa gag 200
Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val Gln Glu

```

15	20	25	30	
gat gtg cag cca cca ggg tta aaa gtg tgg tct gat cca ttt ggc agg				248
Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe Gly Arg				
	35	40	45	
aaa tgagagggct gtcacagct ctgattaaga aaggagattt cttcatgctt				301
Lys				
tcgattctgc atggggtaca gccagtcacc tcaccagaga atgacggctg gagaagaaaa				361
ctctgtaata ccataaataa gagtgcttgt aataaaagac tgtgcacaag gattaatatt				421
tcccttctta agtatcaaaa gaactctgga acaaattata ccattaggaa ggttttcatg				481
attcagttga ttttccaaaa atgaagctat ctcacccagc tgggtttgga ggagcaatct				541
gcttattatt ctgtcgttac cacttactca agcgagctgt gatatgaata caagcaacca				601
gtgggctcgg gaaggtccgg gtctcttctg ccatcttcca gataagagat ttcagtaaaa				661
aactgccatg ctgagctgcc ttatagagct cttcgaaaat gttcgagttg ataaagctct				721
ttgaggacaa ggtacttcgt gcacctcatg ctgaagattg caccatgttg gaagataaat				781
atgaagcaag tcaactaga tgcatacact tgtgtagaaa tcaataatca attaatagaa				841
gtgaaaaaat agacattaag atgattttatt tccactttgc aaaaaaaaaa aaaa				895

<210> 43
 <211> 691
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..613

<220>
 <221> sig_peptide
 <222> 20..82
 <223> Von Heijne matrix
 score 10
 seq LWALAMVTRPASA/AP

<400> 43	
ataccttaga ccctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc	52
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala	
-20 -15	
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca	100
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro	
-10 -5 1 5	
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg	148
Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu	
10 15 20	
cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga tgg	196
Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Trp	
25 30 35	
ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa	244
Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu	
40 45 50	
ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt	292
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu	
55 60 65 70	
cgg gca agc ctg ttg gag act cag atg gag gag gat att ctg cag ctg	340
Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu	
75 80 85	
cag gca gag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca cag	388
Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln	

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          90          95          100
aag gtg cta cgg gac agc gtg cag cgg cta gaa gtc cag ctg agg agc      436
Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser
          105          110          115
gcc tgg ctg ggc cct gcc tac cga gaa ttt gag gtc tta aag gct cac      484
Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His
          120          125          130
gct gac aag cag agc cac atc cta tgg gcc ctc aca ggc cac gtg cag      532
Ala Asp Lys Gln Ser His Ile Leu Trp Ala Leu Thr Gly His Val Gln
          135          140          145          150
cgg cag agg cgg gag atg gtg gca cag cag cat cgg ctg cga cag atc      580
Arg Gln Arg Arg Glu Met Val Ala Gln Gln His Arg Leu Arg Gln Ile
          155          160          165
cag gag aga ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac      633
Gln Glu Arg Leu His Thr Ala Ala Leu Pro Ala
          170          175
tgaggaccaa tcatgctgca aggaacactt ccacgccccg tgaggccct gtgcaggg      691

<210> 44
<211> 458
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..416

<220>
<221> sig_peptide
<222> 12..86
<223> Von Heijne matrix
      score 4
      seq LVVMVPLVGLIHL/GW

<220>
<221> polyA_signal
<222> 425..430

<220>
<221> polyA_site
<222> 445..458

<220>
<221> misc_feature
<222> 201
<223> n=a, g, c or t

<400> 44
gctgaagtac t atg agc ctt cgg aac ttg tgg aga gac tac aaa gtt ttg      50
      Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu
          -25          -20          -15
gtt gtt atg gtc cct tta gtt ggg ctc ata cat ttg ggg tgg tac aga      98
Val Val Met Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg
          -10          -5          1
atc aaa agc agc cct gtt ttc caa ata cct aaa aac gac gac att cct      146
Ile Lys Ser Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro
      5          10          15          20

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gag caa gat agt ctg gga ctt tca aat ctt cag aag agc caa atc cag	194
Glu Gln Asp Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln	
25 30 35	
ggg aag nta gca ggc ttg caa tct tca ggt aaa gaa gca gct ttg aat	242
Gly Lys Xaa Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn	
40 45 50	
ctg agc ttc ata tcg aaa gaa gag atg aaa aat acc agt tgg att aga	290
Leu Ser Phe Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg	
55 60 65	
aag aac tgg ctt ctt gta gct ggg ata tct ttc ata ggt gac cat ctt	338
Lys Asn Trp Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu	
70 75 80	
gga aca tac ttt ttg cag agg tct gca aag cag tct gta aaa ttt cag	386
Gly Thr Tyr Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln	
85 90 95 100	
tct caa agc aaa caa aag agt att gaa gag tgaagtaaaa taaatatttg	436
Ser Gln Ser Lys Gln Lys Ser Ile Glu Glu	
105 110	
gaattactaa aaaaaaaaaa aa	458

<210> 45

<211> 2036

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 276..1040

<220>

<221> sig_peptide

<222> 276..485

<223> Von Heijne matrix

score 3.9

seq SVIGVMLAPFTAG/LS

<220>

<221> polyA_site

<222> 2024..2036

<400> 45

gatcctgggt gcagctcatc acaagcgtcg gggcgcagca aaaccatcca ggctggacag	60
tggctggaca gttccaagaa aagaaacgct tcaccgaaga agtcattgaa tacttccaga	120
agaaagttag cccagtgcac ctgaaaatcc tgctgactag cgatgaagcc tggaagagat	180
tcgtgcgtgt ggctggattg cccaggggaag aagcagatgc tctctatgaa gctctgaaga	240
atcttacacc atatgtggct attgaggaca aagac atg cag caa aaa gaa cag	293
Met Gln Gln Lys Glu Gln	
-70 -65	
cag ttt agg gag tgg ttt ttg aaa gag ttt cct caa atc aga tgg aag	341
Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile Arg Trp Lys	
-60 -55 -50	
att cag gag tcc ata gaa agg ctt cgt gtc att gca aat gag att gaa	389
Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn Glu Ile Glu	
-45 -40 -35	
aag gtc cac aga ggc tgc gtc atc gcc aat gtg gtg tct ggc tcc act	437
Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser Gly Ser Thr	
-30 -25 -20	

ggc atc ctg tct gtc att ggc gtt atg ttg gca cca ttt aca gca ggg	485
Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe Thr Ala Gly	
-15 -10 -5	
ctg agc ctg agc att act gca gct ggg gta ggg ctg gga ata gca tct	533
Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly Ile Ala Ser	
1 5 10 15	
gcc acg gct ggg atc gcc tcc agc atc gtg gag aac aca tac aca agg	581
Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr Tyr Thr Arg	
20 25 30	
tca gca gaa ctc aca gcc agc agg ctg act gca acc agc act gac caa	629
Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser Thr Asp Gln	
35 40 45	
ttg gag gca tta agg gac att ctg cat gac atc aca ccc aat gtg ctt	677
Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro Asn Val Leu	
50 55 60	
tcc ttt gca ctt gat ttt gac gaa gcc aca aaa atg att gcg aat gat	725
Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile Ala Asn Asp	
65 70 75 80	
gtc cat aca ctc agg aga tct aaa gcc act gtt gga cgc cct ttg att	773
Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg Pro Leu Ile	
85 90 95	
gct tgg cga tat gta cct ata aat gtt gtt gag aca ctg aga aca cgt	821
Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu Arg Thr Arg	
100 105 110	
ggg gcc ccc acc cgg ata gtg aga aaa gta gcc cgg aac ctg ggc aag	869
Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn Leu Gly Lys	
115 120 125	
gcc act tca ggt gtc ctc gtt gtg ctg gat gta gtc aac ctt gtg caa	917
Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn Leu Val Gln	
130 135 140	
gac tca ctg gac ttg cac aag ggg gaa aaa tcc gag tct gct gag ttg	965
Asp Ser Leu Asp Leu His Lys Gly Glu Lys Ser Glu Ser Ala Glu Leu	
145 150 155 160	
ctg agg cag tgg gct cag gag ctg gag gag aat ctc aat gag ctc acc	1013
Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn Glu Leu Thr	
165 170 175	
cat atc cat cag agt cta aaa gca ggc taggcccaat tgttgcgga	1060
His Ile His Gln Ser Leu Lys Ala Gly	
180 185	
agtcagggac cccaaacgga gggactggct gaagccatgg cagaagaacg tggattgtga	1120
agatttcatg gacatttatt agttcccaa attaatattt ttataatttc ctatgcctgt	1180
ctttaccgca atctctaaac acaaattgtg aagatttcat ggacacttat cacttcccca	1240
atcaataccc ttgtgatttc ttatgcctgt ctttacttta atctcctaata cctgtcagct	1300
gaggaggggtg tatgtcacct caggaccatg tgataattgc gttaactgca caaattgtag	1360
agcatgtgtg tttgaacaat atgaaatctg ggcaccttga aaaaagaaca ggataacagc	1420
aatcgttcag gggataagag agataacctt aaactctgac caacagttag cgggtggag	1480
cagagtcata tttcttttct ttcaaaagca aatgggagaa atatcgctga attctttttc	1540
tcagcaagga acatccctga gaaagagaat gcacccctga ggggtgggtct ataaatggcc	1600
tccttgggtg tggccatctt ctatggtcga gactgtaggg atgaaataaa cccagtcctc	1660
ccatagtgtc cccaggctta ttaggaagag gaaattccc cctaataaat tttggtcaga	1720
ccggttgctc tcaaaaccct gtctcctgat aagatgttat caatgacaat ggtgcctgaa	1780
acctcattag caattttaat ttctccccgg tcctgtgggtc ctgtgatctc acctgcctc	1840
cacttgctt gtgatattct attaccttgt gaagtaggtg atctttgtga cccacacct	1900
attcatacac tcctccctt tttggaagtc cctaataaaa acttgctgggt tttgcagctt	1960
gtgaggcatc acggaaccta ctgatgtgtg atgtctcccc tggacaccta gctttaaaat	2020
ttcaaaaaaa aaaaaa	2036

<210> 46
 <211> 1276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 443..619

<220>
 <221> sig_peptide
 <222> 443..589
 <223> Von Heijne matrix
 score 7
 seq LICVVCLYIVCRC/GS

<220>
 <221> polyA_site
 <222> 1267..1276

<400> 46
 gaggcactca cggcatttca ttgctacttt aatttttcatt attatgggat tgattgctgt 60
 cacagctact gctgcagtag ctggagttgc tttgcattcc acagtacaaa cagcagacta 120
 tgtaaataat tggtagaaaa attctactct gctgtggaat taccaagata atatagacca 180
 gaaactagct gatcaaatta atgatctcca acaaaactgta atgtggctag gggatcatat 240
 agttagttta gaatatagaa tgcggttaca atgtgattga aatacctctg atttttgcat 300
 tactctcat ctgtgtaatg aaacagagca tgagtgggaa aaagttaaga gatattttaa 360
 aggtcatact agaaatttat ctttggatat tgcaaagcta aaggaacaag tatttcaagc 420
 ccctcagata catctgacac ta atg cca gga act gaa gtg ctt gaa gga gct 472
 Met Pro Gly Thr Glu Val Leu Glu Gly Ala
 -45 -40
 aca gac gga tta gca gct att aac ctg cta aaa tgg atc aag aca ctt 520
 Thr Asp Gly Leu Ala Ala Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu
 -35 -30 -25
 gga ggc tct gtg att tca atg att gtg ctt tta atc tgt gtt gtt tgt 568
 Gly Gly Ser Val Ile Ser Met Ile Val Leu Leu Ile Cys Val Val Cys
 -20 -15 -10
 ctt tat ata gtc tgt aga tgc gga agc cac ctc tgg aga gaa agc cac 616
 Leu Tyr Ile Val Cys Arg Cys Gly Ser His Leu Trp Arg Glu Ser His
 -5 1 5
 cac tgagagcaag caatgatagc tgtggcggtt ttgcaaaaag aaaagggaga 669
 His
 10
 caagcgccca gctatagtta ccaataaagc atggtactgg tattaaaata ggcattgtgt 729
 ctgttccaat ggaacagaat agagaacca gaaacaaagc caaatattta cagccaactg 789
 atctctgaca aagcaacaa aaacataaag tggggaaagg acaccctatt ccacaaatag 849
 tgcagggata attggcaagc cacatgtaga aaaatgaagc tggatcctcg tctctcactt 909
 tatacaaaaa tcaactcaaa atgggtcaaa gtcttaactc taagacctga aaccataaca 969
 attctagaaa ataacattgg aaaaactctt ctagacattg gtttaggcaa aaagttcatg 1029
 accaagaacc caaaagcaaa tgcaataaaa aggaagataa atagatggga cctaattaag 1089
 ctgaaaagct tctgcatagc aaaaggaata atcagcagag caaacagaca acccacaggg 1149
 tgggagaaaa tatttgcaag ctatgtatct gacaatggac taatatccag aatctacaag 1209
 gaattcaaac aattagcaag aaaaaacact tgtatttgtt ttgctctgta aatcagcaaa 1269
 aaaaaaa 1276

<210> 47
 <211> 747

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 206..745

<400> 47

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accagaagca ggtgatttcc gagctcagca atgctcagct cataatgatg tcaagcacca      60
tgccagttt tatgaatggc ttctgtgtc taatgaccct gacaacccat gttcactcaa      120
gtgccaagcc aaaggaacaa ccctggttgt tgaactagca cctaaggtct tagatggtag      180
gcgttgctat acagaatctt tggat atg tgc atc agt ggt tta tgc caa att      232
                               Met Cys Ile Ser Gly Leu Cys Gln Ile
                               1           5

ggt ggc tgc gat cac cag ctg gga agc acc gtc aag gaa gat aac tgt      280
Val Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys
10           15           20           25
ggg gtc tgc aac gga gat ggg tcc acc tgc cgg ctg gtc cga ggg cag      328
Gly Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln
           30           35           40
tat aaa tcc cag ctg tcc gca acc aaa tgc gat gat act gtg gtt gca      376
Tyr Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala
           45           50           55
att ccc tat gga agt aga cat att cgc ctt gtc tta aaa ggt cct gat      424
Ile Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp
           60           65           70
cac tta tat ctg gaa acc aaa acc ctg cag ggg act aaa ggt gaa aac      472
His Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn
           75           80           85
agt ctg agc tcc aca gga act ttc ctt gtg gac aat tct agt gtg gac      520
Ser Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp
           90           95          100          105
ttc cag aaa ttt cca gac aaa gag ata ctg aga atg gct gga cca ctg      568
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu
           110          115          120
aca gca gat ttc att gtc aag att cgt aac tgc ggc tcc gct gac agt      616
Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser
           125          130          135
aca gtc cag ttc atc ttc tat caa ccc atc atc cac cga tgg agg gag      664
Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu
           140          145          150
acg gat ttc ttt cct tgc tca gca acc tgt gga gga ggt tat cag ctg      712
Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu
           155          160          165
aca tgc gct gag tgc tac gat ctg agg agc aac cg      747
Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn
170           175          180

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<210> 48
 <211> 561
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..521

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<220>
<221> sig_peptide
<222> 36..104
<223> Von Heijne matrix
      score 7.4
      seq VLLLAALPPVLLP/GA

<220>
<221> polyA_signal
<222> 528..533

<220>
<221> polyA_site
<222> 548..561

<400> 48
gacgcctctt tcagcccggg atcgccccag caggg atg ggc gac aag atc tgg      53
                               Met Gly Asp Lys Ile Trp
                               -20
ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg      101
Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu
      -15                               -10                               -5
cct ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt      149
Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe
      1                               5                               10                               15
acc ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg      197
Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu
      20                               25                               30
aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta      245
Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu
      35                               40                               45
gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt      293
Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe
      50                               55                               60
gaa caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt      341
Glu Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly
      65                               70                               75
gat tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag      389
Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys
      80                               85                               90                               95
gtg att ttc ttt gaa tta atc ccg gat aat atg gga gaa cag gca caa      437
Val Ile Phe Phe Glu Leu Ile Pro Asp Asn Met Gly Glu Gln Ala Gln
      100                               105                               110
gaa caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat      485
Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp
      115                               120                               125
atg aaa ctg gaa gac atc ctg gtc agt atg gtc ttc taataaaata      531
Met Lys Leu Glu Asp Ile Leu Val Ser Met Val Phe
      130                               135
aaaattatta acagccaaaa aaaaaaaaaa      561

<210> 49
<211> 632
<212> DNA
<213> Homo sapiens

<220>

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<222> 21..41

<220>

<221> polyA_signal

<222> 328..333

<220>

<221> polyA_site

<222> 357..370

<400> 50

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ctgggacttc tggcctcaca atg gtt gag atg act ggg gtg tagcagtgcc      51
                        Met Val Glu Met Thr Gly Val
                        1           5
```

```
aagtcgaggc tgtgaaaggc cttccacctt tactctcgtg ctcgtgccct cccccattgt      111
taggagaagg gcatgctcag gccagcccat tagcccagga ggaggacaag aaacacacgg      171
agcagacaca agccacctca ccaaccacgc caaggctgtc ctgaattagc aaccctgaca      231
cgtgtgagca agtccaacgg acaccggaag atccacctag tcaagcccaa ccaagactgg      291
cagagctgcc aagctgacca cttaaggcgc atgaggaata aacactcgtt gctgcatgcc      351
attgcaaaaa aaaaaaaaaa                                     370
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<210> 51

<211> 994

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 35..631

<220>

<221> sig_peptide

<222> 35..160

<223> Von Heijne matrix

score 8.6

seq ASLFLLLSLTVFS/IV

<220>

<221> polyA_signal

<222> 901..906

<220>

<221> polyA_site

<222> 979..994

<400> 51

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ataattggag ctgcaaagca gatcgtgaca agag atg gac ggt cag aag aaa aat      55
                        Met Asp Gly Gln Lys Lys Asn
                        -40
```

```
tgg aag gac aag gtt gtt gac ctc ctg tac tgg aga gac att aag aag      103
Trp Lys Asp Lys Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys
-35           -30           -25           -20
```

```
act gga gtg gtg ttt ggt gcc agc cta ttc ctg ctg ctt tca ttg aca      151
Thr Gly Val Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr
-15           -10           -5
```

```
gta ttc agc att gtg agc gta aca gcc tac att gcc ttg gcc ctg ctc      199
Val Phe Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu
```

	1		5		10	
tct gtg acc atc agc ttt agg ata tac aag ggt gtg atc caa gct atc						247
Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile						
15		20		25		
cag aaa tca gat gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa						295
Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu						
30	35	40	45			
ggt cat gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt						343
Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu						
50	55	60				
ggt cat gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt						391
Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val						
65	70	75				
gat gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt						439
Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe						
80	85	90				
acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg gct						487
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala						
95	100	105				
ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat cag gca						535
Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His Gln Ala						
110	115	120	125			
cag ata gat cat tat cta gta ctt gca aat aag aat gtt aaa gat gct						583
Gln Ile Asp His Tyr Leu Val Leu Ala Asn Lys Asn Val Lys Asp Ala						
130	135	140				
atg gct aaa atc caa gca aaa atc cct gga ttg aag cgc aaa gct gaa						631
Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu						
145	150	155				
tgaaaacgcc caaataatt agtaggagtt catcttttaa ggggatattc atttgattat						691
acggggggagg gtcaggaag aacgaacctt gacgttgcag tgcagtttca cagatcggtg						751
ttagatcttt atttttagcc atgcactggt gtgaggaaaa attacctgtc ttgactgcc						811
tgtgttcac atcttaagta ttgtaagctg ctatgtatgg atttaaaccg taatcatatc						871
tttttcctat ctatctgagg cactgggtgga ataaaaaacc tgtatatttt actttgttgc						931
agatagtctt gccgcatctt ggcaagttgc agagatgggtg gagctagaaa aaaaaaaac						991
aaa						994

<210> 52
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 271..399

<400> 52	
gccgctagcg cctcgagcga tgcacctcct ttccaactgg gcaaaccctcg cttccagcag	60
acgtcctttct atggccgctt caggcacttc ttggatatca tgcacctcgc cacactcttt	120
gtcactgaga gacgtctcag agaggctgtg cagctgctgg aggactataa gcatgggacc	180
ctgcgcccgg gggtcaccaa tgaacagctc tggagtgcac agaaaatcaa gcaggctatt	240
ctacatccgg acaccaatga gaagatcttc atg cca ttt aga atg tca ggt tat	294
Met Pro Phe Arg Met Ser Gly Tyr	

	1		5	
att cct ttt ggg acg cca att gta agt gtt acc ttc aaa gga ttt cct				342
Ile Pro Phe Gly Thr Pro Ile Val Ser Val Thr Phe Lys Gly Phe Pro				
10	15	20		
ttt cta aaa aat tat ttt aaa tgt cta act tta tgt tat tgc tca cgg				390

Phe Leu Lys Asn Tyr Phe Lys Cys Leu Thr Leu Cys Tyr Cys Ser Arg
25 30 35 40
gta ttt gac tgaattggtt att 412
Val Phe Asp

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<210> 53
<211> 597
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 103..252
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<220>
<221> sig_peptide
<222> 103..213
<223> Von Heijne matrix
      score 3.9
      seq PGPSLRRLFSGSQA/SV
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<220>
<221> polyA_site
<222> 588..597
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[illegible]

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<210> 54
<211> 748
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 2..460

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<220>
<221> polyA signal
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<222> 713..718

<220>

<221> polyA_site

<222> 735..748

<400> 54

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c aca gtt cct ctc ctc cta gag cct gcc gac cat gcc cgc ggg cgt gcc      49
  Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
    1           5           10          15
cat gtc cac cta cct gaa aat gtt cgc agc cag tct cct ggc cat gtg      97
His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
           20           25           30
cgc agg ggc aga agt ggt gca cag gta cta ccg acc gga cct gat gag      145
Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
           35           40           45
aaa cag gtt gag aag agt gaa gtt gat ttc tca aag tca cat agc tta      193
Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
           50           55           60
gtg aga cga ttt gag gat ctg aag ccc aag ctt tct gtt tgc aaa act      241
Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
           65           70           75           80
gga tca caa gtc ttt cgg tgc gag aac tgg aag gtc tgg gca gag tgc      289
Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
           85           90           95
agc aga gga gac cat gat gac tgc cta gac ttg tgc tca gtg ctg tgt      337
Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
           100          105          110
tgg gga gaa ctg cta cgg aca ata cct gaa att cca cca aag cgt gga      385
Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
           115          120          125
gaa ctc aaa acg gag ctt ttg gga ctg aaa gaa aga aaa cac aaa cct      433
Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
           130          135          140
caa gtt tct caa cag gag gaa ctt aaa taactatgcc aagaattctg      480
Gln Val Ser Gln Gln Glu Leu Lys
           145          150
tgaataatat aagtcttaaa tatgtatttc ttaatttatt gcatcaaact acttgctcct      540
aagcacttag tctaagtcta actgcaagag gaggtgctca gtggatgttt agccgatacg      600
ttgaaattta attacggttt gattgatatt tcttgaaaac cgccaaagca catatcatca      660
aaccatttca tgaatatggt ttggaagatg tttagtcttg aatataatgc gaaatagaat      720
atttgtaagt ctaccaaaaa aaaaaaaaaa      748
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<210> 55

<211> 703

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..231

<220>

<221> polyA_signal

<222> 769..774

<220>

<221> polyA_site

<222> 690..703

<400> 55

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ctctggtggc tctgctacgg cggcgcagaa atg agg cag aag cgg aaa gga gat      54
                               Met Arg Gln Lys Arg Lys Gly Asp
                               1           5
ctc agc cct gct aag ctg atg atg ctg act ata gga gat gtt att aaa      102
Leu Ser Pro Ala Lys Leu Met Met Leu Thr Ile Gly Asp Val Ile Lys
   10           15           20
caa ctg att gaa gcc cac gag cag ggg aaa gac atc gat cta aat aag      150
Gln Leu Ile Glu Ala His Glu Gln Gly Lys Asp Ile Asp Leu Asn Lys
   25           30           35           40
gtg aga acc aag aca gct gcc aaa tat ggc ctt tct gcc cag ccc cgc      198
Val Arg Thr Lys Thr Ala Ala Lys Tyr Gly Leu Ser Ala Gln Pro Arg
               45           50           55
ctg gtg gat atc att gct gcc gtc cct cct gag tagctgggat tacaggcacc      251
Leu Val Asp Ile Ile Ala Ala Val Pro Pro Glu
               60           65
cgccgctgcc aatttttcta ttttttagtag ggatgggggt ttcaccatat tggtcaggct      311
ggtctcgaac tcctgacctc aggtgatcaa cccaccttgg cctccctaaa tgccgggatt      371
acaggcatga gccaccgctc cgggcctttg attttttaag gtggattttg gttgttataa      431
atggagaaaag gtaagagttc aagttcaacc cgtgtgtgaa agcaaaaaca tggaaaacag      491
gattggcttc ttcaaaggct cctctttaga aactgcctct ttgaaatttc gaggtaatct      551
actttggaga ctctgcctgg agagggtcag ttcctaagtt aaaagcatcg cttaaccttg      611
gctcctgtgg cattttacaa aggtttaaag gaattgattc ctctgaaagg gcctgaaaat      671
aaaaagtctt taacatacaa aaaaaaaaaa aa      703
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<210> 56

<211> 725

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 305..565

<220>

<221> polyA_signal

<222> 694..699

<220>

<221> polyA_site

<222> 713..725

<400> 56

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ctcacggttg tgaaggtcac aggggttcag cactcccagt agaccaggag ctccgggagg      60
cagggccggc cccacgtcct ctgcgcacca cctgagttg gatcctctgt gcgccacccc      120
tgagttggat ccagggttag ctgctgttga cctccccact cccacgctgc cctcctgcct      180
gcagccatga cgcccctgct caccctgatc ctggtggtcc tcatgggctt acctctggcc      240
caggccttgg actgccacgt gtgaggacta caaatccctc caggatatca ttgccatcct      300
gggt atg gat gaa ctt tct gag gaa gac aag ttg acc gtg tcc cgt gca      349
      Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala
      1           5           10           15
cgg aaa ata cag cgt ttc ttg tct cag cca ttc cag gtt gct gag gtc      397
Arg Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val
      20           25           30
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ttc aca ggt cat atg ggg aag ctg gta ccc ctg aag gag acc atc aaa	445
Phe Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys	
35 40 45	
gga ttc cag cag att ttg gca ggt gaa tat gac cat ctc cca gaa cag	493
Gly Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln	
50 55 60	
gcc ttc tat atg gtg gga ccc att gaa gaa gct gtg gca aaa gct gat	541
Ala Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp	
65 70 75	
aag ctg gct gaa gag cat tca tcg tgaggggtct ttgtcctctg tactgtctct	595
Lys Leu Ala Glu Glu His Ser Ser	
80 85	
ctccttgccc ctaacccaaa aagcttcatt tttctgtgta ggctgcacaa gagccttgat	655
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 score 3.6
 seq HLSVVTIAAKVKC/IP

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gtg atg agt gcg gaa gtg aag gtg aca ggg cag aac cag gag caa ttt	168
Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe	
-85 -80 -75	
ctg ctc cta gcc aag tcg gcc aag ggg gca gcg ctg gcc aca ctc atc	216
Leu Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile	
-70 -65 -60 -55	
cat cag gtg ctg gag gcc cct ggt gtc tac gtg ttt gga gaa ctg ctg	264
His Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu	
-50 -45 -40	

gac atg ccc aat gtt aga gag ctg naa gcc cgg aat ctt cct cca cta	312
Asp Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu	
-35 -30 -25	
aca gag gct cag aag aat aag ctt cga cac ctc tca gtt gtc acc ctg	360
Thr Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu	
-20 -15 -10	
gct gct aaa gta aag tgt atc cca tat gca gtg ttg ctg gag gct ctt	408
Ala Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu	
-5 1 5 10	
gcc ctg cgt aat gtg cgg cag ctg gaa gac ctt gtg att gag gct gtg	456
Ala Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val	
15 20 25	
tat gct gac gtg ctt cgt ggc tcc ctg gac cag cgc aac cag cgg ctc	504
Tyr Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu	
30 35 40	
gag gtt gac tac agc atc ggg cgg gac atc cag cgc cag gac ctc agt	552
Glu Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser	
45 50 55	
gcc att gcc cga acc ctg cag gaa tgg tgt gtg ggc tgt gag gtc gtg	600
Ala Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val	
60 65 70	
ctg tca ggc att gag gag cag gtg agc cgt gcc aac caa cac aag gag	648
Leu Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu	
75 80 85 90	
cag cag ctg ggc ctg aag cag cag att gag agt gag gtt gcc aac ctt	696
Gln Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu	
95 100 105	
aaa aaa acc att aaa gtt acg acg gca gca gca gcc gca gcc aca tct	744
Lys Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Ala Ala Thr Ser	
110 115 120	
cag gac cct gag caa cac ctg act gag ctg agg gaa cca gct cct ggc	792
Gln Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly	
125 130 135	
acc aac cag cgc cag ccc agc aag aaa gcc tca aag ggc aag ggg ctc	840
Thr Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu	
140 145 150	
cga ggg agc gcc aag att tgg tcc aag tcg aat tgaaagaact gtcgtttcct	893
Arg Gly Ser Ala Lys Ile Trp Ser Lys Ser Asn	
155 160 165	
ccctgggggat gtgggggtccc agctgcctgc ctgcctctta ggagtcctca gagagccttc	953
tggtcccctg gccagctgat aatcctaggt tcatgaccct tcacctcccc taaccccaaa	1013
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agtgggaaag ggaa atg ccg acc aat tgc gct gcg gcg ggc tgt gcc act      170
          Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr
                    1             5             10
acc tac aac aag cac att aac atc agc ttc cac agg taacctgggc      216
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg
          15             20
agggagtggg ggtgacggaa actggagttc ctattgtggc tatcgcttgt gtggaaggaa      276
caggaggatt ctgctaattc taataacttt cccagctggg agcaggggaag catcgatatgt      336
cctttgtgtt tctcaaactc gcccaattgt tctctgcttt cggggaagct ttactcattt      396
tctaaaagaa atccaagtac tgtttggtca ttacccttta gtaaaaaaaaa gtaacaggag      456
gatatcgtaa ttttctactg ttttattcct ctgttagacc gggccttgac atgaatgacg      516
ccgtaaggga gaaagagatc ttcccaatca gcaatcaccg taaaagcctg ctgtgttccc      576
gttaaaatta ggaaattctc actagatgaa ttgacatggg aggcatttag atttctaata      636
gtcacatagt aattctgcgg aggaattgag tcatctttga tagccatgga attaagcgat      696
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cctagggtttt cttttgtttg ctggaagaaa aatcaaaatt ctttagttct gtcaaaccag      816
aactcttgaa agcactttga acaatgcctg gaaaataaca ggtactctgt aaatgtttac      876
cttctctgca agtgccctgc acgtgcccga agaaaagaca cattaaaaag ttaagtgaca      936
ccagtccctga ttttatatat tttatatacc taacaacgta tatgttagta tgtagaaatt      996
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aaaaaaaaaa aaa                                         1069
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<222> 1071..1084

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agtgggaaag ggaa atg ccg acc aat tgc gct gcg gcg ggc tgt gcc act      170
                Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr
                1                5                10
acc tac aac aag cac att aac atc agc ttc cac agg ttt cct ttg gat      218
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp
                15                20                25
cct aaa aga aga aaa gaa tgg gtt cgc ctg gtt agg cgc aaa aat ttt      266
Pro Lys Arg Arg Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe
                30                35                40
gtg cca gga aaa cac act ttt ctt tgt tca aag cac ttt gaa gcc tcc      314
Val Pro Gly Lys His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser
                45                50                55                60
tgt ttt gac cta aca gga caa act cga cga ctt aaa atg gat gct gtt      362
Cys Phe Asp Leu Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val
                65                70                75
cca acc att ttt gat ttt tgt acc cat ata aag tct atg aaa ctc aag      410
Pro Thr Ile Phe Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys
                80                85                90
tca agg aat ctt ttg aag aaa aac agt tgt tct cca gct gga cca      458
Ser Arg Asn Leu Leu Lys Lys Asn Ser Cys Ser Pro Ala Gly Pro
                95                100                105
tct agt tta aaa tca aac att agt agt cag caa gta cta ctt gaa cac      506
Ser Ser Leu Lys Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His
                110                115                120
agc tat gcc ttt agg aat cct atg gag gca aaa aag agg atc att aaa      554
Ser Tyr Ala Phe Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys
                125                130                135                140
ctg gaa aaa gaa ata gca agc tta aga aga aaa atg aaa act tgc cta      602
Leu Glu Lys Glu Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu
                145                150                155
caa aag gaa cgc aga gca act cga aga tgg atc aaa gcc atg tgt ttg      650
Gln Lys Glu Arg Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu
                160                165                170
gta aag aat tta gaa gca aat agt gta tta cct aaa ggt aca tca gaa      698
Val Lys Asn Leu Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu
                175                180                185
cac atg tta cca act gcc tta agc agt ctt cct ttg gaa gat ttt aag      746
His Met Leu Pro Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys
                190                195                200
atc ctt gaa caa gat caa caa gat aaa aca ctg cta agt cta aat cta      794
Ile Leu Glu Gln Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu
                205                210                215                220
aaa cag acc aag agt acc ttc att taaatttagc ttgcacagag cttgatgcct      848
Lys Gln Thr Lys Ser Thr Phe Ile
                225
atccttcatt cttttcagaa gtaaagataa ttatggcact tatgccaaaa ttcattatct      908
aataaagttt tacttgaagt aacattactg aatttgtgaa gacttgatta caaaagaata      968
aaaaacttca tatggaaatt ttatttgaaa atgagtggaa ggccttaca ttagaattac      1028
ggacttaaaa attttgctaa taaattgtgt gtttgaaagg tgaaaaaaaa aaaaaa      1084

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 tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca cct ttc 101
 Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro Pro Phe
 -10 -5 1
 tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt agg cta 149
 Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys Arg Leu
 5 10 15
 tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc tgt tta 197
 Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr Cys Leu
 20 25 30 35
 tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa aat tgt 245
 Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys Asn Cys
 40 45 50
 aat agt cgg cac gct gga ttt gta ggg cca gca aaa ttg cgg cag 290
 Asn Ser Arg His Ala Gly Phe Val Gly Pro Ala Lys Leu Arg Gln
 55 60 65
 tgaaactagt ttcacttcta aagcccttca tttccacaa ggtaagctc tcgaaacccc 350
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 gtatgcaaa 419

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 <222> 485..616

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 <222> 669..682

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 tattttattg atcacatctt taatcttttg ttctctatac gtggcctgtt ttgatttatt 180
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 ctcatattt ttggcagtaa gcatttctct tttattgctt tctatgtagt ctttaatttt 360
 gcttttaact tcttctttga tctaaggatt acctacttgt taatttccaa atattatctt 420
 atctatctat ctatctatct atctatctat ctatctatct acctatgtga gacgaagtct 480
 ggct atg tcg ccg agg ctg gag tgc agt ggt gca atc ttg gct cac tgc 529

Met	Ser	Pro	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Leu	Ala	His	Cys	
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aac	ccc	cgc	ctc	cca	ggt	tca	agt	tat	tct	cct	gcc	tca	gct	act	tgg
Asn	Pro	Arg	Leu	Pro	Gly	Ser	Ser	Tyr	Ser	Pro	Ala	Ser	Ala	Thr	Trp
			20					25					30		
gtg	aga	gga	tcc	ctt	gag	ccg	ggg	agg	ttg	agg	ctg	cag	tgagccataa		
Val	Arg	Gly	Ser	Leu	Glu	Pro	Gly	Arg	Leu	Arg	Leu	Gln			
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577

626

682

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 seq LVHHCPTWQWATG/EE

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Gln	Asn	Val	Ile	Asn	Thr	Val	Lys	Gly	Lys	Ala	Leu	Glu	Val	Ala	Glu
	-55						-50					-45			
tac	ctg	acc	ccg	gtc	ctc	aag	gaa	tca	aag	ttt	agg	gaa	aca	ggt	gta
Tyr	Leu	Thr	Pro	Val	Leu	Lys	Glu	Ser	Lys	Phe	Arg	Glu	Thr	Gly	Val
	-40					-35					-30				
att	acc	cca	gaa	gag	ttt	gtg	gca	gct	gga	gat	cac	cta	gtc	cac	cac
Ile	Thr	Pro	Glu	Glu	Phe	Val	Ala	Ala	Gly	Asp	His	Leu	Val	His	His
	-25				-20				-15				-10		
tgt	cca	aca	tgg	caa	tgg	gct	aca	ggg	gaa	gaa	ttg	aaa	gtg	aag	gca
Cys	Pro	Thr	Trp	Gln	Trp	Ala	Thr	Gly	Glu	Glu	Leu	Lys	Val	Lys	Ala
			-5					1				5			
tac	cta	cca	aca	ggc	aaa	caa	ttt	ttg	gta	acc	aaa	aat	gtg	ccg	tgc
Tyr	Leu	Pro	Thr	Gly	Lys	Gln	Phe	Leu	Val	Thr	Lys	Asn	Val	Pro	Cys
	10					15				20					
tat	aag	cgg	tgc	aaa	cag	atg	gaa	tat	tca	gat	gaa	ttg	gaa	gct	atc
Tyr	Lys	Arg	Cys	Lys	Gln	Met	Glu	Tyr	Ser	Asp	Glu	Leu	Glu	Ala	Ile
	25				30					35					
att	gaa	gaa	gat	gat	ggt	gat	ggc	gga	tgg	gta	gat	aca	tat	cac	aac
Ile	Glu	Glu	Asp	Asp	Gly	Asp	Gly	Gly	Trp	Val	Asp	Thr	Tyr	His	Asn

56

104

152

200

248

296

344

392

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aat aag gac aat ata agg ctt caa gat tgc tca gca cta tgt gaa gag	488						
Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu Glu							
		75		80		85	
gaa gaa gat gaa gat gaa gga gaa gct gca gat atg gaa gaa tat gaa	536						
Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr Glu							
		90		95		100	
gag agt gga ttg ttg gaa aca gat gag gct acc cta gat aca agg aaa	584						
Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg Lys							
		105		110		115	
ata gta gaa gct tgt aaa gcc aaa act gat gct ggc ggt gaa gat gct	632						
Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp Ala							
		120		125		130	
att ttg caa acc aga act tat gac ctt tac atc act tat gat aaa tat	680						
Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys Tyr							
		140		145		150	
tac cag act cca cga tta tgg ttg ttt ggc tat gat gag caa cgg cag	728						
Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg Gln							
		155		160		165	
cct tta aca gtt gag cac atg tat gaa gac atc agt cag gat cat gtg	776						
Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His Val							
		170		175		180	
aag aaa aca gtg acc att gaa aat cat cct cat ctg cca cca cct ccc	824						
Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro Pro							
		185		190		195	
atg tgt tca gtt cac cca tgc agg cat gct gag gtg atg aag aaa atc	872						
Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys Ile							
		200		205		210	
att gag act gtt gca gaa gga ggg gga gaa ctt gga gtt cat atg tat	920						
Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met Tyr							
		220		225		230	
ctt ctt att ttc ttg aaa ttt gta caa gct gtc att cca aca ata gaa	968						
Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile Glu							
		235		240		245	
tat gac tac aca aga cac ttc aca atg taatgaagag agcataaaat	1015						
Tyr Asp Tyr Thr Arg His Phe Thr Met							
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tattcatcaa tatatacagt ttctctaata agggacttat atgtttatgc attaaataaa	1135						
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score 3.5
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tgccgcgctg tcagactcca tccctcctct gccgccaccg cagcagccac aggtag atg 659
Met
-80
agg aca agg acg act ggg aat cct agg ggg ctc cat gac acc ttc ccc 707
Arg Thr Arg Thr Thr Gly Asn Pro Arg Gly Leu His Asp Thr Phe Pro
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cgc aga ccc aga ctt ggc cgt tgc tct gac atg gac aca gcc agg aca 755
Arg Arg Pro Arg Leu Gly Arg Cys Ser Asp Met Asp Thr Ala Arg Thr
-60 -55 -50
agc tgc tca gac ctg ctt ccc tgg gag ggg gtg acg gaa cca gca ctg 803
Ser Cys Ser Asp Leu Leu Pro Trp Glu Gly Val Thr Glu Pro Ala Leu
-45 -40 -35
tgt gga gac cag ctt caa gga acg gaa ggc tgg ctt gag gcc aca cag 851
Cys Gly Asp Gln Leu Gln Gly Thr Glu Gly Trp Leu Glu Ala Thr Gln
-30 -25 -20
ctg ggg cgg gga ctt ctg tct gcc tgt gct cca tgg ggg gac ggc tcc 899
Leu Gly Arg Gly Leu Leu Ser Ala Cys Ala Pro Trp Gly Asp Gly Ser
-15 -10 -5 1
acc cag cct gtg cca ctg tgt tct taagaggctt ccagagaaaa cggcacacca 953
Thr Gln Pro Val Pro Leu Cys Ser
5
atcaataaag aactgagcag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaan 1008

<210> 64
<211> 568
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 18..311

<220>

<221> sig_peptide

<222> 18..62

<223> Von Heijne matrix

score 8.4

seq AMWLLCVALAVLA/WG

<400> 64

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agtgctgctt acccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      50
                Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                -15                -10                -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      98
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
                1                5                10
atg aag agt cgg gag cag gga gga cgg ctg gga gcc gaa agc cgg acc      146
Met Lys Ser Arg Glu Gln Gly Gly Arg Leu Gly Ala Glu Ser Arg Thr
                15                20                25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc      194
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
                30                35                40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      242
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45                50                55                60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa ggt ctt      290
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu
                65                70                75
acc tct gaa ccc ctc aca gcc tagggacagg agcggccggc ttacctggtg      341
Thr Ser Glu Pro Leu Thr Ala
                80
ggttggggga cgtcggcagc tcgctacta cgccagcagg attgaggagc agagaaacag      401
ttgcagttgg ttgtattcag tacctgcatt tccgttggga actccacctg tacttgttat      461
tctgtggaac tttttttatt tgtagaagga gcaagaatat tgaccttact atatagcaca      521
cgaaacaatc tatgctgtat cgtgctgtct caatccttaa agttaac      568
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<210> 65

<211> 538

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 151..426

<220>

<221> sig_peptide

<222> 151..258

<223> Von Heijne matrix

score 5.2

seq KVALAGLLGFGLG/KV

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<222> 505..510

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<222> 527..538

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catggcttca gcgtctgctc gtggaaacca agataaagat gcccatTTTC caccaccaag      120
caagcagctc tgcctTTTTc tcttgtaagc atg ctt gtc acc cag gga cta gtc      174
                               Met Leu Val Thr Gln Gly Leu Val
                               -35                               -30
tac caa ggt tat ttg gca gct aat tct aga ttt gga tca ttg ccc aaa      222
Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys
                               -25                               -20                               -15
ggt gca ctt gct ggt ctc ttg gga ttt ggc ctt gga aag gta tca tac      270
Val Ala Leu Ala Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr
                               -10                               -5                               1
ata gga gta tgc cag agt aaa ttc cat ttt ttt gaa gat cag ctc cgt      318
Ile Gly Val Cys Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg
5                               10                               15                               20
ggg gct ggt ttt ggt cca cag cat aac agg cac tgc ctc ctt acc tgt      366
Gly Ala Gly Phe Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys
                               25                               30                               35
gag gaa tgc aaa ata aag cat gga tta agt gag aag gga gac tct cag      414
Glu Glu Cys Lys Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln
                               40                               45                               50
cct tca gct tcc taaattctgt gtctgtgact ttcgaagttt tttaaacctc      466
Pro Ser Ala Ser
                               55
tgaatttgta cacattttaa atttcaagtg tacttttaaaa taaaatactt ctaatggaac      526
aaaaaaaaaa aa      538

<210> 66
<211> 1747
<212> DNA
<213> Homo sapiens

<220>
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<222> 10..1062

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<222> 10..57
<223> Von Heijne matrix
      score 4.9
      seq FIY LQA HFT L C S G / W S

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<222> 1710..1715

<220>
<221> polyA_site
<222> 1735..1747

<220>
<221> misc_feature
<222> 1011

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<223> n=a, g, c or t

<400> 66

gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt	51
Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys	
-15 -10 -5	
tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg	99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val	
1 5 10	
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta	147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val	
15 20 25 30	
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc	195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala	
35 40 45	
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc	243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly	
50 55 60	
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg	291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro	
65 70 75	
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc	339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu	
80 85 90	
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa	387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu	
95 100 105 110	
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac	435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His	
115 120 125	
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg	483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp	
130 135 140	
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg	531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu	
145 150 155	
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt	579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser	
160 165 170	
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc	627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val	
175 180 185 190	
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc	675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe	
195 200 205	
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg	723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp	
210 215 220	
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac	771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn	
225 230 235	
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg	819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val	
240 245 250	
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca	867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser	
255 260 265 270	

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cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc      915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
      275      280      285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc      963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
      290      295      300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc ccn      1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
      305      310      315
ttt tgt cac ctt gga cat gga aga ctg tgg cta caa cat tcc aca gac      1059
Phe Cys His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp
      320      325      330
aga tgagtcaacc ctcatgacca tagcctatgt catggctgcc atctgogccc      1112
Arg
335
tcttcatgct gccactctgc ctcatgggtgt gtcagtggcg ctgcctccgc tgccctgogcc      1172
agcagcatga tgactttgct gatgacatct ccctgctgaa gtgaggaggc ccatgggcag      1232
aagataggga ttccccctgga ccacacctcc gtggttccact ttggtcacaa gtaggagaca      1292
cagatggcac ctgtggccag agcacctcag gaccctcccc acccaccaaa tgccctctgcc      1352
ttgatggaga aggaaaaggc tggcaagggtg gggtccagggt actgtacctg taggagacag      1412
aaaagagaag aaagaagcac tctgctggcg ggaatactct tggtcacctc aaatttaagt      1472
cgggaaattc tgctgcttga aacttcagcc ctgaaccttt gtcaccattc ctttaaattc      1532
tccaacccaa agtattcttc ttttcttagt ttcagaagta ctggcatcac acgcagggtta      1592
ccttggcggtg tgtccctgtg gtaccctggc agagaagaga ccaagcttgt ttccctgctg      1652
gccaaagtca gtaggagagg atgcacagtt tgctatttgc tttagagaca gggactgtat      1712
aaacaagcct aacattggtg caaaaaaaaa aaaaa      1747

<210> 67
<211> 1686
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..491

<220>
<221> sig_peptide
<222> 78..218
<223> Von Heijne matrix
      score 5.8
      seq LMCFGALIGLCAC/IC

<220>
<221> polyA_signal
<222> 1652..1657

<220>
<221> polyA_site
<222> 1673..1686

<400> 67
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cactaactga gcagtttc atg gag aaa ttt gtt gat ccc gga aac cac aat      110
      Met Glu Lys Phe Val Asp Pro Gly Asn His Asn
      -45      -40
agc ggg att gat ctc ctt agg acc tat ctt tgg cgt tgc cag ttc ctt      158

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Ser	Gly	Ile	Asp	Leu	Leu	Arg	Thr	Tyr	Leu	Trp	Arg	Cys	Gln	Phe	Leu	
-35						-30					-25					
tta	cct	ttt	gtg	agt	tta	ggt	ttg	atg	tgc	ttt	ggg	gct	ttg	atc	gga	206
Leu	Pro	Phe	Val	Ser	Leu	Gly	Leu	Met	Cys	Phe	Gly	Ala	Leu	Ile	Gly	
-20					-15					-10				-5		
ctt	tgt	gct	tgc	att	tgc	cga	agc	tta	tat	ccc	acc	att	gcc	acg	ggc	254
Leu	Cys	Ala	Cys	Ile	Cys	Arg	Ser	Leu	Tyr	Pro	Thr	Ile	Ala	Thr	Gly	
				1				5					10			
att	ctc	cat	ctc	ctt	gca	ggt	ctg	tgt	aca	ctg	ggc	tca	gta	agt	tgt	302
Ile	Leu	His	Leu	Leu	Ala	Gly	Leu	Cys	Thr	Leu	Gly	Ser	Val	Ser	Cys	
		15					20					25				
tat	ggt	gct	gga	att	gaa	cta	ctc	cac	cag	aaa	cta	gag	ctc	cct	gac	350
Tyr	Val	Ala	Gly	Ile	Glu	Leu	Leu	His	Gln	Lys	Leu	Glu	Leu	Pro	Asp	
		30				35					40					
aat	gta	tcc	ggt	gaa	ttt	gga	tgg	tcc	ttc	tgc	ctt	gct	tgt	gtc	tct	398
Asn	Val	Ser	Gly	Glu	Phe	Gly	Trp	Ser	Phe	Cys	Leu	Ala	Cys	Val	Ser	
45					50					55				60		
gct	ccc	tta	cag	ttc	atg	gct	tct	gct	ctc	ttc	atc	tgg	gct	gct	cac	446
Ala	Pro	Leu	Gln	Phe	Met	Ala	Ser	Ala	Leu	Phe	Ile	Trp	Ala	Ala	His	
				65				70				75				
acc	aac	cgg	aga	gag	tac	acc	tta	atg	aag	gca	tat	cgt	gtg	gca		491
Thr	Asn	Arg	Arg	Glu	Tyr	Thr	Leu	Met	Lys	Ala	Tyr	Arg	Val	Ala		
			80					85				90				
tgagcaagaa	actgcctgct	ttacaattgc	cattttttatt	ttttttaa	aat	aatactgata										551
ttttcccccac	ctctcaattg	tttttaattt	ttatttgtgg	atataccatt	ttattatgaa											611
aatctattttt	atttatacac	attcaccact	aaatacacac	ttaataccac	taaaatttat											671
gtgggtttact	ttaagcgatg	ccatctttca	aataaaactaa	tctaggtcta	gacagaaaga											731
aatggataga	gacttgacac	aaatttatga	aagaaaattg	ggagtaggaa	tgtgaccgaa											791
aacaagttgt	gctaagtgtc	gtagactttt	tcagtaaaac	caaagtaact	gtatctgttc											851
aactaaaaaac	tctatattag	tttctttggg	aaacctctca	tcgtcaaaac	tttatgttca											911
ctttgctgtt	gtagatagcc	agtcaaccag	cagtattagt	gctgttttca	aagatttaag											971
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tctgaggtga	gatatggcag	ctgtttgtat	ctgcactgtg	tctgtctaca	aagagtga											1091
aatacagtg	ttacttgaaa	ttttaacttt	gtaactgcaa	gaattccagt	tcggccgggc											1151
gaggattagt	attattttta	actctccgta	agatttttcag	taccaccaa	ttgttttgg											1211
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tattacagtt	acaaggtaaa	attcctcaac	tgctatttat	ttattccagc	ccagtactat											1331
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ttccttgct	aaatcccttc	ctgggtgtga	tcaacattat	ttaatgtctt	ctaattcagt											1511
cattttttat	aagtatgtct	ataaacattg	aactttaaaa	aacttattta	tttattccac											1571
tactgtagca	attgacagat	taaaaaaatg	taacttcata	atttcttacc	ataacctcaa											1631
tgtctttttt	aaaaaataaa	attaaaaatg	aaaagagacc	caaaaaaaaaa	aaaaa											1686

<210> 68
 <211> 542
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..371

<220>
 <221> sig_peptide
 <222> 69..287
 <223> Von Heijne matrix

score 4
seq AVGFLFWIVLTS/WI

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<222> 510..515

<220>
<221> polyA_site
<222> 530..542

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gcgagct atg aac ctg gag cga gtg tcc aat gag gag aaa ttg aac ctg 110
Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu
-70 -65 -60
tgc cgg aag tac tac ctg ggg ggg ttt gct ttc ttg cct ttt ctc tgg 158
Cys Arg Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp
-55 -50 -45
ttg gtc aac atc ttc tgg ttc tac cga gag gcc ttc ctt gtc cca gcc 206
Leu Val Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala
-40 -35 -30
tac aca gaa cag agc caa atc aaa ggc tat gtc tgg cgc tca gct gtg 254
Tyr Thr Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val
-25 -20 -15
ggc ttc ctc ttc tgg gtg ata gtg ctc acc tcc tgg atc acc atc ttc 302
Gly Phe Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe
-10 -5 1 5
cag atc tac cgg ccc cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc 350
Gln Ile Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe
10 15 20
acc ata ccc ctg ggc acc ccc tgacaacttc tgcacatact ggggacctgc 401
Thr Ile Pro Leu Gly Thr Pro
25
ttattctccc aggacaggct ccttaaagca gaggagcctg tcttgggagc cccttctcaa 461
actcctaaga cttgtttctca tgtcccacgt tctctgctga catcccccaa taaaggaccc 521
taactttcaa aaaaaaaaaa a 542

<210> 69
<211> 1174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..757

<220>
<221> sig_peptide
<222> 2..205
<223> Von Heijne matrix
score 7.3
seq LRLILSPLPGAQP/QQ

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<222> 1160..1174

<400> 69

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gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc	97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val	
-50 -45 -40	
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca	145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser	
-35 -30 -25	
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct	193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro	
-20 -15 -10 -5	
ggg gcc cag cct caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc	241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly	
1 5 10	
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat	289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His	
15 20 25	
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta	337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu	
30 35 40	
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag	385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys	
45 50 55 60	
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc	433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe	
65 70 75	
agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc	481
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro	
80 85 90	
atc tgc gag gcc ctc ctg gac cag agg ttc ttc aat ggc att ggc aac	529
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn	
95 100 105	
tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag	577
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu	
110 115 120	
aag gcc cgc tcg gtc ctg gag gcc ctg cag cag cac agg ccg agc ccg	625
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro	
125 130 135 140	
gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat tca gac	673
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp	
145 150 155	
ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggt	721
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly	
160 165 170	
gag gcc aaa gat ggc agc aac ctc tgc ttc agc aaa tgattgtgta	767
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys	
175 180	
accctggggc acttgcccc ctctggacct gattcaccga tttggaagtt tgtagcccta	827
gctgatactc aatggactag gcctcctcac ttgtcaatag tgtttccagg ctgggcgcag	887
tggctcatgc ctgtgggtccc ggcacttcgg gagggccgagt ggggtgggtc acctgaggtc	947
aggagttcga gaccatcctg gccaacatgg tgaaacccca tctccactaa aatgcaaaaa	1007
attagccagg tgtggtggcg ggcacctgta gtctcagcta ctcgaggagga tgaggcagga	1067
aaatcgcttg aaccacaggag gtggagggtt cagttgagct gagatcgtgc cattgcactc	1127
cagcctgggc aacgagagca aaactccatc tcaaaaaaaa aaaaaaa	1174

<210> 70
 <211> 1285
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 2..1051

<220>
 <221> sig_peptide
 <222> 2..205
 <223> Von Heijne matrix
 score 7.3
 seq LRLILSPLPGAQP/QQ

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 <222> 1248..1253

<220>
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 <222> 1272..1285

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 gcc tgc agg gcg ctg gtg ttc ggc gcc tgc gtg gag aag tcc tct gtc 97
 Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
 agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca 145
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
 gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct 193
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
 -20 -15 -10 -5
 ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc 241
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
 1 5 10
 atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat 289
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
 15 20 25
 gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta 337
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
 tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag 385
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
 45 50 55 60
 tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc 433
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 agg ctg aag atc ccc ccc ttt gag aag gcc cgc tcg gtc ctg gag gcc 481
 Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala
 80 85 90
 ctg cag cag cac agg ccg agc ccg gag ctg acc ctg agc cag aag ata 529

Leu	Gln	Gln	His	Arg	Pro	Ser	Pro	Glu	Leu	Thr	Leu	Ser	Gln	Lys	Ile	
	95						100					105				
agg	acc	aag	ctg	cag	aat	cca	gac	ctg	ctg	gag	cta	tgt	cac	tca	gtg	577
Arg	Thr	Lys	Leu	Gln	Asn	Pro	Asp	Leu	Leu	Glu	Leu	Cys	His	Ser	Val	
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ccc	aag	gaa	gtg	gac	cag	ttg	ggg	ggc	agg	ggc	tac	ggg	tca	gag	agc	625
Pro	Lys	Glu	Val	Asp	Gln	Leu	Gly	Gly	Arg	Gly	Tyr	Gly	Ser	Glu	Ser	
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ggg	gag	gag	gac	ttt	gct	gcc	ttt	cga	gcc	tgg	ctg	cgc	tgc	tat	ggc	673
Gly	Glu	Glu	Asp	Phe	Ala	Ala	Phe	Arg	Ala	Trp	Leu	Arg	Cys	Tyr	Gly	
				145				150						155		
atg	cca	ggc	atg	agc	tcc	ctg	cag	gac	cgg	cat	ggc	cgt	acc	atc	tgg	721
Met	Pro	Gly	Met	Ser	Ser	Leu	Gln	Asp	Arg	His	Gly	Arg	Thr	Ile	Trp	
		160						165					170			
ttc	cag	ggg	gat	cct	gga	ccg	ttg	gca	ccc	aaa	ggg	cgc	aag	tcc	cgc	769
Phe	Gln	Gly	Asp	Pro	Gly	Pro	Leu	Ala	Pro	Lys	Gly	Arg	Lys	Ser	Arg	
	175					180					185					
aaa	aag	aaa	tcc	aag	gcc	aca	cag	ctg	agt	cct	gag	gac	aga	gtg	gag	817
Lys	Lys	Lys	Ser	Lys	Ala	Thr	Gln	Leu	Ser	Pro	Glu	Asp	Arg	Val	Glu	
	190				195					200						
gac	gct	ttg	cct	cca	agc	aag	gcc	cct	tcc	aag	aca	cga	agg	gca	aag	865
Asp	Ala	Leu	Pro	Pro	Ser	Lys	Ala	Pro	Ser	Lys	Thr	Arg	Arg	Ala	Lys	
205					210					215					220	
aga	gac	ctt	cct	aag	agg	act	gca	acc	cag	cgg	cct	gag	ggg	acc	agc	913
Arg	Asp	Leu	Pro	Lys	Arg	Thr	Ala	Thr	Gln	Arg	Pro	Glu	Gly	Thr	Ser	
				225					230					235		
ctc	cag	cag	gac	cca	gaa	gct	ccc	aca	gtg	ccc	aag	aag	ggg	agg	agg	961
Leu	Gln	Gln	Asp	Pro	Glu	Ala	Pro	Thr	Val	Pro	Lys	Lys	Gly	Arg	Arg	
			240				245						250			
aag	ggg	cga	cag	gca	gcc	tct	ggc	cac	tgc	aga	ccc	cgg	aag	gtc	aag	1009
Lys	Gly	Arg	Gln	Ala	Ala	Ser	Gly	His	Cys	Arg	Pro	Arg	Lys	Val	Lys	
	255					260				265						
gct	gac	atc	cca	tcc	ttg	gaa	cca	gag	ggg	acc	tca	gcc	tct			1051
Ala	Asp	Ile	Pro	Ser	Leu	Glu	Pro	Glu	Gly	Thr	Ser	Ala	Ser			
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ggtctgaatt	tttgggagca	ggcaatatct	gaagggtgcaa	acaggcccta	cggctgttcc											1171
ctgcacaact	ctcatggttt	taattgtacc	ccatcttcca	catctttaaa	gctcatgtga											1231
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score 7.3

seq LRLILSPLPGAQP/QQ

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gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc	97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val	
-50 -45 -40	
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca	145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser	
-35 -30 -25	
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct	193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro	
-20 -15 -10 -5	
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc	241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly	
1 5 10	
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat	289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His	
15 20 25	
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctg gcc cta	337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu	
30 35 40	
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Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys	
45 50 55 60	
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc	433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe	
65 70 75	
agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc	481
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro	
80 85 90	
atc tgc gag gcc ctg ctg gac cag agg ttc ttc aat ggc att ggc aac	529
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn	
95 100 105	
tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag	577
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu	
110 115 120	
aag gcc cgc tcg gtc ctg gag gcc ctg cag cag cac agg ccg agc ccg	625
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro	
125 130 135 140	
gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat cca gac	673
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp	
145 150 155	
ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggg	721
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly	
160 165 170	
ggc aga ggc tac ggg tca gag agc ggg gag gag gac ttt gct gcc ttt	769
Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe	
175 180 185	
cga gcc tgg ctg cgc tgc tat ggc atg cca ggc atg agc tcc ctg cag	817

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Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln
190                195                200
gac cgg cat ggc cgt acc atc tgg ttc cag ggg gat cct gga ccg ttg      865
Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu
205                210                215                220
gca ccc aaa ggg cgc aag tcc cgc aaa aag aaa tcc aag gcc aca cag      913
Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln
                225                230                235
ctg agt cct gag gac aga gtg gag gac gct ttg cct ccg agc aag gcc      961
Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
                240                245                250
cct tcc agg aca cga agg gca aag aga gac ctt cct aag agg act gca      1009
Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
                255                260                265
acc cag cgg cct gag ggg acc agc ctc cag cag gac cca gaa gct ccc      1057
Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
                270                275                280
aca gtg ccc aag aag ggg agg agg aag ggg cga cag gca gcc tct ggc      1105
Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
285                290                295                300
cac tgc aga ccc cgg aag gtc aag gct gac atc cca tcc ttg gaa cca      1153
His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
                305                310                315
gag ggg acc tca gcc tct tagcaggagg ctctccttgc ttgcactcac      1201
Glu Gly Thr Ser Ala Ser
                320
cctttcttat tgtcttgccc tgcattctggg ggtctgaatt tttgggagca ggcaatatct      1261
gaagggtgcaa acaggcccta cggctgttcc ctgcacaact ctcatggttt taattgtacc      1321
ccatcttcca catctttaaa gctcatgtga aaaatgctgc atttttaata aactgatata      1381
tttgaaaaaa aaaaaaa      1398

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<223> Von Heijne matrix
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tgt gct gtg gtc ctg gcc cag tac ctt tgg ttt cac aga aga tct ctg						104
Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe His Arg Arg Ser Leu						
	-75			-70		-65
cca ggc aag gcc atc tta gag att gga gca gga gtg agc ctt cca gga						152
Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly Val Ser Leu Pro Gly						
	-60			-55		-50
att ttg act gcc aaa tgt ggt gca gaa gta ata ctg tca gac agc tca						200
Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile Leu Ser Asp Ser Ser						
	-45			-40		-35
gaa ctg cct cac tgt ctg gaa gtc tgt cgg caa agc tgc caa atg aat						248
Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln Ser Cys Gln Met Asn						
			-25		-20	-15
aac ctg cca cat ctg cag gtg gta gga cta aca tgg ggt cat ata tct						296
Asn Leu Pro His Leu Gln Val Val Gly Leu Thr Trp Gly His Ile Ser						
		-10		-5		1
tgg gat ctt ctg gct cta cca cca caa gat att atc ctt gca tct gat						344
Trp Asp Leu Leu Ala Leu Pro Gln Asp Ile Ile Leu Ala Ser Asp						
	5		10		15	
gtg ttc ttt gaa cca gaa gat ttt gaa gac att ttg gct aca ata tat						392
Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile Leu Ala Thr Ile Tyr						
	20		25		30	35
ttt ttg atg cac aag aat ccc aag gtc caa ttg tgg tct act tat caa						440
Phe Leu Met His Lys Asn Pro Lys Val Gln Leu Trp Ser Thr Tyr Gln						
		40		45		50
gtt agg agt gct gac tgg tca ctt gaa gct tta ctc tac aaa tgg gat						488
Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu Leu Tyr Lys Trp Asp						
	55		60		65	
atg aaa tgt gtc cac att cct ctt gag tct ttt gat gca gac aaa gaa						536
Met Lys Cys Val His Ile Pro Leu Glu Ser Phe Asp Ala Asp Lys Glu						
	70		75		80	
gat ata gca gaa tct acc ctt cca gga aga cat aca gtt gaa atg ctg						584
Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His Thr Val Glu Met Leu						
	85		90		95	
gtc att tcc ttt gca aag gac agt ctc tgaattatac ctacaacctg						631
Val Ile Ser Phe Ala Lys Asp Ser Leu						
	100		105			
ttctgggaca gtatcaatac tgatgagcaa cctggcacac aaactatgag cagaccactt						691
cagcttgaga atgcagtggg tctgaagatg gtcaagtctg tctgccttag attttgatgt						751
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aaaaaaaaaa						821

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 score 4.2

seq LVTPAALRPLVLG/GN

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<222> 904..916

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  Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
    -230                -225                -220

gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta      157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
  -215                -210                -205

tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc      205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
  -200                -195                -190                -185

gta cac ttg atg ggg gac aac tta tgc aat gat ggc tct ctc ctg ctc      253
Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
    -180                -175                -170

caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc      301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
    -165                -160                -155

ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg      349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
    -150                -145                -140

ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att      397
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
    -135                -130                -125

cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag      445
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
    -120                -115                -110                -105

gta gaa tgg ata ttt tca gga cgg cgc gca aag gag gag att gta ttt      493
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
    -100                -95                -90

cgt tac tac cac aaa ctc agg atg tct gcg gag tac tcc cag agc tgg      541
Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
    -85                -80                -75

ggc cac ttc cag aat cgt gtg aac ctg gtg ggg gac att ttc cgc aat      589
Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn
    -70                -65                -60

gac ggt tcc atc atg ctt caa gga gtg agg gag tca gat gga gga aac      637
Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
    -55                -50                -45

tac acc tgc agt atc cac cta ggg aac ctg gtg ttc aag aaa acc att      685
Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
    -40                -35                -30                -25

gtg ctg cat gtc agc ccg gaa gag cct cga aca ctg gtg acc ccg gca      733
Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
    -20                -15                -10

gcc ctg agg cct ctg gtc ttg ggt ggt aat cag ttg gtg atc att gtg      781
Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
    -5                1                5

gga att gtc tgt gcc aca atc ctg ctg ctc cct gtc ctg ata ttg atc      829
Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
    10                15                20

gtg aag aag acc tgt gga aat aag agt tca gtg aat tct aca gtc ttg      877

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Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
 25 30 35 40 916
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 Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta 157
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc 205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc 253
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc 301
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg 349
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att 397
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
 100 105 110
 cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag 445
 Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
 115 120 125
 gta gaa tgg ata ttt tca gga cgg cgc gca aag gta aca agg agg aaa 493
 Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
 130 135 140
 cat cac tgt gtt aga gaa ggc tct ggc tgatggtatc aggacaaagg 540
 His His Cys Val Arg Glu Gly Ser Gly
 145 150
 tagaatcagg cacatgagga ggtgttgcaa gagcctgggc tttggtgctt atcagaactg 600
 gaccttctcc tagcaatttc agctttctgg tgggaaaggt aactccaatg aagaacaaga 660

acaagaagat	gatgatgatg	cttaactttt	tggatgccga	tatgagattg	tacatgtaaa	720
gcatttttcta	taagactttg	cccctgcatt	ttagttttcct	tctttctccc	ttttccttcg	780
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ctgtgcccc	ttgccccatt	tatgtgatgg	agggaaattt	catgggtact	tcacgtgttg	960
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aaaaaaaaaa	aaa					1153

attgtcctcc ttgttatttc tgtttgtaag acttaagtga gttaggtctt taaggaaagc 1457
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Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu Gly Gly Val
-10 -5 1
aat aaa att gcg gag aag ata tgt gga gac ctg aaa gat ccc tgc aaa 147
Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys
5 10 15
ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt aga tat ttc 195
Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe Arg Tyr Phe
20 25 30
tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc tcc ggc tgt 243
Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe Ser Gly Cys
35 40 45 50
aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt gaa gta gcc 291
Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg Glu Val Ala
55 60 65
tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg tgaactcatg 338
Cys Val Ala Lys Tyr Lys Pro Pro Arg
70 75
aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcagactg attttgaaat 398
ctttgtaata tttccataat gctttaagct tccatatggt tgctattttc ctgaccctag 458
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<223> Von Heijne matrix

score 5.6

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Lys Pro Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala	
-20 -15 -10	
ctt ttg cga tta gga gat acc aaa aaa aag cga cag cct gaa gca gcc	145
Leu Leu Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala	
-5 1 5	
aca aaa tcc tgt gtt aga agc agc tgt ggg ggt ccc agt gga gat ggg	193
Thr Lys Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly	
10 15 20 25	
cct ccc cca tgc ctc cag cag cct gac cct cgt gcc ctg tct cag gcg	241
Pro Pro Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala	
30 35 40	
ttc tct aga tcc ttt cct ctg ttt ccc tct ctc gct ggc aaa agt atg	289
Phe Ser Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met	
45 50 55	
atc taattgaaac aagactgaag gatcaataaa cagccatctg ccccttcaaa	342
Ile	
aaaaaaaaaa	352

<210> 78

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 16..378

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<221> sig_peptide

<222> 16..84

<223> Von Heijne matrix

score 9.8
seq FLLFFFLFLLTRG/SL

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<222> 502..507

<220>

<221> polyA_site

<222> 522..542

<400> 78

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cacgacctgt gggcc atg atg cta ccc caa tgg ctg ctg ctg ctg ttc ctt      51
          Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu
                    -20                    -15

ctc ttc ttc ttt ctc ttc ctc ctc acc agg ggc tca ctt tct cca aca      99
Leu Phe Phe Phe Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr
   -10           -5           1           5
aaa tat aac ctt ttg gag ctc aag gag tct tgc atc cgg aac cag gac      147
Lys Tyr Asn Leu Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp
                10                15                20
tgc gag act ggc tgc tgc caa cgt gct cca gac aat tgc gag tgc cac      195
Cys Glu Thr Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
                25                30                35
tgc gcg gag aag ggg tcc gag ggc agt ctg tgt caa acg cag gtg ttc      243
Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe
                40                45                50
ttt ggc caa tat aga gcg tgt ccc tgc ctg cgg aac ctg act tgt ata      291
Phe Gly Gln Tyr Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile
                55                60                65
tat tca aag aat gag aaa tgg ctt agc atc gcc tat ggc cgt tgt cag      339
Tyr Ser Lys Asn Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln
                70                75                80                85
aaa att gga agg cag aag ttg gct aag aaa atg ttc ttc tagtgctccc      388
Lys Ile Gly Arg Gln Lys Leu Ala Lys Lys Met Phe Phe
                90                95
tccttcttgc tgcttctctc tcctccacct gctctctctc ctaccagag ctctgtgttc      448
accctgttcc ccagagcctc caccatgagt ggagggaagt ggggagtgat tgaaataaag      508
agctttttca atgaaaaaaaa aaaaaaaaaa aaaa      542

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<210> 79

<211> 233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..233

<400> 79

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gcaaaaccaa aaccagcacc gatcccgaca tagatcagtg acgtcttttt cttcag atg      59
                                   Met
                                   1
atc cta tgt ttc ctt ctt cct cat cat cgt ctt cag gaa gcc aga cag      107
Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg Gln
                5                10                15
att caa gta ttg aag atg ctg cca agg gaa aaa tta aga aga aga gaa      155

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Ile	Gln	Val	Leu	Lys	Met	Leu	Pro	Arg	Glu	Lys	Leu	Arg	Arg	Arg	Glu		
	20						25				30						
gag	aga	aaa	caa	ata	aat	ggg	aaa	aaa	gaa	agg	aca	aaa	tat	gaa	aca	203	
Glu	Arg	Lys	Gln	Ile	Asn	Gly	Lys	Lys	Glu	Arg	Thr	Lys	Tyr	Glu	Thr		
	35					40					45						
cca	aga	aaa	aga	gaa	gga	aaa	aaa	aaa	aaa							233	
Pro	Arg	Lys	Arg	Glu	Gly	Lys	Lys	Lys	Lys								
50					55												

<210> 80
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 <222> 83..124
 <223> Von Heijne matrix
 score 7.5
 seq VALNLIILVPCCAA/WC

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 <222> 573..578

<220>
 <221> polyA_site
 <222> 607..660

<400> 80																	
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gagaggggag	atcactcttt	tg atg gtg gcc	ctg aac ctc	att ctg gtt	ccc											112	
		Met Val Ala	Leu Asn	Leu Ile	Leu Val	Pro											
				-10		-5											
tgc tgc gct	gct tgg tgt	gac cca	cgg agg	atc cac	tcc cag	gat gac										160	
Cys Cys Ala	Ala Trp Cys	Asp Pro	Arg Arg	Ile His	Ser Gln	Asp Asp											
	1		5		10												
gtg ccc cgt	agc tct gct	gct gat	act ggg	tct gcg	atg cag	cgg cgt										208	
Val Pro Arg	Ser Ser Ala	Ala Asp	Thr Gly	Ser Ala	Met Gln	Arg Arg											
	15		20		25												
gag gcc tgg	gct ggt tgg	aga agg	tca caa	ccc ttc	tct gtt	ggt ctg										256	
Glu Ala Trp	Ala Gly Trp	Arg Arg	Ser Gln	Pro Phe	Ser Val	Gly Leu											
	30		35		40												
cct tct gct	gaa aga ctc	gag aac	caa cca	ggg aag	ctg tcc	tgg agg										304	
Pro Ser Ala	Glu Arg Leu	Glu Asn	Gln Pro	Gly Lys	Leu Ser	Trp Arg											
	45		50		55												
tcc ctg gtc	gga gag gga	tat aga	atc tgt	gac ctc	tgacaactgt											350	
Ser Leu Val	Gly Glu Gly	Tyr Arg	Ile Cys	Asp Leu													
	65		70														
gaagccaccc	tgggctacag	aaaccacagt	cttcccagca	attattacaa	ttcttgaatt											410	
ccttggggat	tttttactgc	cctttcaaag	cacttaagt	ttagatctaa	cgtgttccag											470	
tgtctgtctg	aggtgactta	aaaaatcaga	acaaaacttc	tattatccag	agtcattggga											530	
gagtacaccc	tttccaggaa	taatgttttg	ggaaacactg	aatgaaatc	ttcccagtat											590	

tataaattgt gtattttaaa aaagaaactt ttctgaatgc ctacctggcg gtgtatacca 650
ggcagtgtgc 660

<210> 81
<211> 605
<212> DNA
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<222> 47..541

<220>
<221> sig_peptide
<222> 47..220
<223> Von Heijne matrix
score 5.4
seq QLLDSVLWL GALG/LT

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<222> 597..605

<400> 81
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Met Thr Arg
ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg atc cca gtt cct 103
Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile Pro Val Pro
-55 -50 -45 -40
cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt cca gtg cgt cca 151
Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro Val Arg Pro
-35 -30 -25
cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc ctg gac agt gtc 199
Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu Asp Ser Val
-20 -15 -10
cta tgg ctg ggg gca cta gga ctg aca atc cag gca gtc ttt tcc acc 247
Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val Phe Ser Thr
-5 1 5
act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc ctc acc ttt gac 295
Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu Thr Phe Asp
10 15 20 25
ctg ctc cat agg ccc gca ggt cac act ctg cca cag cgc aaa ctt ctc 343
Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg Lys Leu Leu
30 35 40
acc agg ggc cag agt cag ggg gcc ggt gaa ggt cct gga cag cag gag 391
Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly Gln Gln Glu
45 50 55
gct cta ctc ctg caa atg ggt aca gtc tca gga caa ctt agc ctc cag 439
Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu Ser Leu Gln
60 65 70
gac gca ctg ctg ctg ctg ctc atg ggg ctg ggc ccg ctc ctg aga gcc 487
Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu Leu Arg Ala
75 80 85
tgt ggc atg ccc ttg acc ctg ctt ggc ctg gct ttc tgc ctc cat cct 535
Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys Leu His Pro
90 95 100 105
tgg gcc tgagagcccc tccccacaac tcagtgtcct tcaaataac aatgaccacc 591

Trp Ala
cttcttcaaa aaaa

605

<210> 82
<211> 396
<212> DNA
<213> Homo sapiens

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<222> 46..285

<220>
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<222> 46..150
<223> Von Heijne matrix
score 3.6
seq LEPGLSSSAACNG/KE

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<221> polyA_signal
<222> 364..369

<220>
<221> polyA_site
<222> 385..396

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Met Pro Phe Gln
-35
ttt gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca 105
Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser
-30 -25 -20
att gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag 153
Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys
-15 -10 -5 1
gag atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc 201
Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys
5 10 15
ctg aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag 249
Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys
20 25 30
cca cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt 295
Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
35 40 45
aagtccttttg tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct 355
ggtaaacaaa taaaagtggg ggcaccttca aaaaaaaaaa a 396

<210> 83
<211> 432
<212> DNA
<213> Homo sapiens

<220>
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<222> 22..240

<220>
 <221> sig_peptide
 <222> 22..84
 <223> Von Heijne matrix
 score 12
 seq VLVLCVLLLQAQG/GY

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 <222> 397..402

<220>
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 <222> 421..432

<400> 83
 gctcacgctc tggtcagagt t atg gca ccc cag act ctg ctg cct gtc ctg 51
 Met Ala Pro Gln Thr Leu Leu Pro Val Leu
 -20 -15
 gtt ctc tgt gtg ctg ctg ctg cag gcc cag gga gga tac cgt gac aag 99
 Val Leu Cys Val Leu Leu Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys
 -10 -5 1 5
 atg agg atg cag aga atc aag gtc tgt gag aag cga ccc agc ata gat 147
 Met Arg Met Gln Arg Ile Lys Val Cys Glu Lys Arg Pro Ser Ile Asp
 10 15 20
 cta tgc atc cac cac tgt tca tgt ttc caa aag tgt gaa aca aat aag 195
 Leu Cys Ile His His Cys Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys
 25 30 35
 ata tgc tgt tca gcc ttc tgt ggg aac att tgt atg agc atc cta 240
 Ile Cys Cys Ser Ala Phe Cys Gly Asn Ile Cys Met Ser Ile Leu
 40 45 50
 tgagtgggag agtgggctgg gatgtgcatc ctgctccctg aacccttcca tccgagactg 300
 tgccacatc cgaagcacia ggacatcaaa tcatcagcac aagaacatca acaggaatgc 360
 caccctcccc agtgtctgaa ctccctgtcc ctgtcaaata aaccagaaca aatgcccata 420
 aaaaaaaaaa aa 432

<210> 84
 <211> 420
 <212> DNA
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<220>
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 <222> 89..382

<220>
 <221> polyA_site
 <222> 408..420

<400> 84
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 ggctggtgct gtaacaaaga cccatgtg atg ctg ggg gca gag aca gag gag 112
 Met Leu Gly Ala Glu Thr Glu Glu
 1 5
 aag ctg ttt gat gcc ccc ttg tcc atc agc aag aga gag cag ctg gaa 160
 Lys Leu Phe Asp Ala Pro Leu Ser Ile Ser Lys Arg Glu Gln Leu Glu

10	15	20	
cag cag gtc cca gag aac tac ttc tat gtg cca gac ctg ggc cag gtg			208
Gln Gln Val Pro Glu Asn Tyr Phe Tyr Val Pro Asp Leu Gly Gln Val			
25	30	35	40
cct gag att gat gtt cca tcc tac ctg cct gac ctg ccc ggc att gcc			256
Pro Glu Ile Asp Val Pro Ser Tyr Leu Pro Asp Leu Pro Gly Ile Ala			
45	50	55	
aac gac ctc atg tac att gcc gac ctg ggc ccc ggc att gcc ccc tct			304
Asn Asp Leu Met Tyr Ile Ala Asp Leu Gly Pro Gly Ile Ala Pro Ser			
60	65	70	
gcc cct ggc acc att cca gaa ctg ccc acc ttc cac act gag gta gcc			352
Ala Pro Gly Thr Ile Pro Glu Leu Pro Thr Phe His Thr Glu Val Ala			
75	80	85	
gag cct ctc aag acc tac aag atg ggg tac taacagcacc accaccgccc			402
Glu Pro Leu Lys Thr Tyr Lys Met Gly Tyr			
90	95		
ccaccaaaaa aaaaaaaa			420

<210> 85
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 80..415

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 <222> 80..142
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 score 5.4
 seq TFCLIFGLGAVWG/LG

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 <222> 471..476

<220>
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 <222> 488..501

<400> 85	
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gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt	112
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys	
-20 -15	
ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc	160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser	
-10 -5 1 5	
cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc	208
Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr	
10 15 20	
gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc	256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu	
25 30 35	
ttt caa gat act ccc aga agc ata aaa gca tcc act gct aca gct gaa	304

Phe	Gln	Asp	Thr	Pro	Arg	Ser	Ile	Lys	Ala	Ser	Thr	Ala	Thr	Ala	Glu	
40						45					50					
cag	ttt	ttt	cag	aag	ctg	aga	aat	aaa	cat	gaa	ttt	act	att	ttg	gtg	352
Gln	Phe	Phe	Gln	Lys	Leu	Arg	Asn	Lys	His	Glu	Phe	Thr	Ile	Leu	Val	
55					60					65				70		
acc	cta	aaa	cag	acc	cac	tta	aat	tca	gga	ggt	att	ctc	tca	att	cac	400
Thr	Leu	Lys	Gln	Thr	His	Leu	Asn	Ser	Gly	Val	Ile	Leu	Ser	Ile	His	
				75					80					85		
cac	ttg	gat	cac	agg	taa	atgtggt	tgctggagtt	tcctgtgttt	tcattatatg							455
His	Leu	Asp	His	Arg												
				90												
tggttaa	aatg	aatatattaa	agagaagtaa	acaaaaaaaa	aaaaaa											501

<210> 86
 <211> 454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..361

<220>
 <221> sig_peptide
 <222> 152..283
 <223> Von Heijne matrix
 score 4.7
 seq FLLSLSLITYCFW/DP

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ttagcgaagt	ccagttttca	gcattttgtc	cttattggac	aatagcaagg	atattagaac											120
gtgttggttc	cgctgtcttc	cgtcttgagt	t atg tgc tgc	tat tgt cgg	ata											172
			Met Cys Cys Tyr Cys Arg Ile													
			-40													
ttt tgt ctt	aga tgt acg	tac ttt cct	ggt cat tgt	ggt atg tgt	aat											220
Phe Cys Leu	Arg Cys Thr	Tyr Phe Pro	Val His Cys	Gly Met Cys	Asn											
	-35		-30		-25											
ttg cgt tac	ttt gaa ttt	tcc acg ttt	tta ctt tct	ttg tct ctc	atc											268
Leu Arg Tyr	Phe Glu Phe	Ser Thr Phe	Leu Leu Ser	Leu Ser Leu	Ile											
	-20		-15		-10											
act tac tgc	ttt tgg gac	ccc ccc cat	cgg ggt tca	cat tcc ctc	tcc											316
Thr Tyr Cys	Phe Trp Asp	Pro Pro His	Arg Gly Ser	His Ser Leu	Ser											
	-5		1		5				10							
cta gag cac	act ccc ttg	gat ttc ctc	gag tgg ggt	ctg ctg cgg												361
Leu Glu His	Thr Pro Leu	Asp Phe Leu	Glu Trp Gly	Leu Leu Arg												
	15		20		25											
tgaagctttc	ccattttatg	tcagattat	tttcagaggg	tatatagaat	tcaggcagct											421
gtttcgttgt	agcacattaa	aatattttc	ccc													454

<210> 87
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 32..307

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<221> sig_peptide

<222> 32..70

<223> Von Heijne matrix

score 4.2

seq MLFSLSLLSNLNQ/IG

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<222> 1240..1245

<220>

<221> polyA_site

<222> 1261..1272

<400> 87

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Met Leu Phe Ser Leu Ser Leu

-10

ctc tcc aac ctt aac caa atc ggc agc agc cac ctc gac cgc cca cac 100

Leu Ser Asn Leu Asn Gln Ile Gly Ser Ser His Leu Asp Arg Pro His

-5

1

5

10

att cct ggc caa tca gct cag ctg ttt att tac caa atg tct tca caa 148

Ile Pro Gly Gln Ser Ala Gln Leu Phe Ile Tyr Gln Met Ser Ser Gln

15

20

25

caa cta cag cag cag cct tcg gct aac aaa aaa gca gga aaa atc cac 196

Gln Leu Gln Gln Gln Pro Ser Ala Asn Lys Lys Ala Gly Lys Ile His

30

35

40

aac acc ccc ttc gcc aac caa cta aat cca acg caa cat ctg gca aaa 244

Asn Thr Pro Phe Ala Asn Gln Leu Asn Pro Thr Gln His Leu Ala Lys

45

50

55

cct ttt cag caa att ctt cct ggc cgt cag tcc ggc agc ctc acc tca 292

Pro Phe Gln Gln Ile Leu Pro Gly Arg Gln Ser Gly Ser Leu Thr Ser

60

65

70

cca ttt cta gct tgc tgaaacccaa aactaatctc caagaaggag aagcttctct 347

Pro Phe Leu Ala Cys

75

cgcagccgga gcaggtccct ttctagagat aggagaagag agagatcgct gtctcgggag 407

agaaatcaca agccgtcccg atccttctct aggtctcgta gtcgatttag gtcaaatagaa 467

aggaaataga agacagtttg caagagaagt ggtgtacagg aaattacttc atttgacagg 527

agtatgtaca gaaaattcaa gttttgtttg agacttcata agcttggtgc atttttaaga 587

tgtttttagct gttcaaattct gtttgtctct tgaaacagtg acacaaaagt gtaattctct 647

atggtttgaa atggatcata cgaggcatgt aataccaaga attgttactt tacaatgttc 707

ccttaagcaa aattgaattt gctttgaact tttagttatg cacagactga taataaacct 767

ctaaacctgc ccagcgggaag tgtgtttttt tttaaattta aatacagaaa caactggcaa 827

aaattgaact aagatttact tttttttcca tagctgggat ataggctgca gctatagttg 887

aacaagcagt ctttaaaaac tgctgtgaaa cacaggccat cagggaaaac gaaatgctgc 947

actattaaat tagaggtttt tgaaaaatcc aactctcatc ctgggcagag gttgcctagt 1007

tggtatagaa tgtaagtgtt caagaaagtt tacctttgct ttaggtcgta agttccttat 1067

ttgattgccg tatatggata catggctgtt cgtgacattc tttatgtgca aatttgtgat 1127

ttcaaaaatg tcctgccagt ttaagggtac attgtagagc cgaactttga gttactgtgc 1187

aagatttttt ttcattgctgt catttgtaat atgttttgtg agaatccttg ggattaaagt 1247

tttggttaca gattaataaaaa aaaaa 1272

<210> 88

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<222> 114..734
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<221> polyA_signal  
<222> 768..773
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agctgccaaa caagtacggg agttctgaaa atccagaatg gcttgatggt tac atg															116
Met															
cac att tta caa ctg ctt act aca gtg gat gat gga att caa gca att	164														
His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile															
-40 -35 -30															
gta cat tgt cct gac act gga aaa gac att tgg aat tta ctt ttt gac	212														
Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp															
-25 -20 -15 -10															
ctg gtc tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt	260														
Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu															
-5 1 5															
caa gaa cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc	308														
Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala															
10 15 20															
atc tat gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta	356														
Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val															
25 30 35															
gat ctt cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa	404														
Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu															
40 45 50 55															
cag tgt cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa	452														
Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu															
60 65 70															
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Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile Leu															
75 80 85															
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Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr															
90 95 100															
aag gag acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag	596														
Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln															
105 110 115															

aag tgt tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg	644
Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val	
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gtg gaa gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct	692
Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala	
140 145 150	
gat gac ttg gaa aaa aac ttc cca agt ttg aag gtt cag act	734
Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr	
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aaaaaaaaaa	804

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tgctgcaaga tctgttatcc gctctgtggt tttgtcatcc ttgctgcctg tgttgtggcc	180
tgtgttggct tgggtgtgg atg cag gtt gct ctc aag gag gat ctg gat gcc	231
Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala	
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ctc aag gaa aaa ttt cga aca atg gaa tct aat cag aaa agc tca ttc	279
Leu Lys Glu Lys Phe Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe	
15 20 25	
caa gaa atc ccc aaa ctt aat gaa gaa cta ctc agc aag caa aaa caa	327
Gln Glu Ile Pro Lys Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln	
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ctt gag aag att gaa tct gga gag atg ggt ttg aac aaa gtc tgg ata	375
Leu Glu Lys Ile Glu Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile	
45 50 55	
aac atc aca gaa atg aat aag cag att tct ctg ttg act tct gca gtg	423
Asn Ile Thr Glu Met Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val	
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Asn His Leu Lys Ala Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu	
80 85 90	
cct acc act gta gag gga ctt cag aag agt gta gct tcc att ggc aat	519
Pro Thr Thr Val Glu Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn	
95 100 105	
act tta aac agc gtc cat ctt gct gtg gaa gca cta cag aaa act gtg	567
Thr Leu Asn Ser Val His Leu Ala Val Glu Ala Leu Gln Lys Thr Val	
110 115 120	

gat gaa cac aag aaa acg atg gaa tta ctg cag agt gat atg aat cag	615
Asp Glu His Lys Lys Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln	
125 130 135	
cac ttc ttg aag gag act cct gga agc aac cag atc att ccg tca cct	663
His Phe Leu Lys Glu Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro	
140 145 150 155	
tca gcc aca tca gaa ctt gac aat aaa acc cac agt gag aat ttg aaa	711
Ser Ala Thr Ser Glu Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys	
160 165 170	
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Gln Met Gly Asp Arg Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln	
175 180 185	
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His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys Ala Ala	
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Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu Gly Glu	
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cca cca gag cac act ctc cgg tac ctg gtc ctc cac cta gcc tcc ctg	199
Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala Ser Leu	
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cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg gct gag gag ctg	247
Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu Glu Leu	
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cgc cac atc cac tcc agg tac cgg ggc agc tac tgg agg act gtg cgg	295

Arg	His	Ile	His	Ser	Arg	Tyr	Arg	Gly	Ser	Tyr	Trp	Arg	Thr	Val	Arg		
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gcc	tgc	ctg	ggc	tgc	ccc	ctc	cgc	cgt	ggg	gcc	ctg	ttg	ctg	ctg	tcc	343	
Ala	Cys	Leu	Gly	Cys	Pro	Leu	Arg	Arg	Gly	Ala	Leu	Leu	Leu	Leu	Ser		
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Ile	Tyr	Phe	Tyr	Tyr	Ser	Leu	Pro	Asn	Ala	Val	Gly	Pro	Pro	Phe	Thr		
				70					75					80			
tgg	atg	ctt	gcc	ctc	ctg	ggc	ctc	tcg	cag	gca	ctg	aac	atc	ctc	ctg	439	
Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	Gln	Ala	Leu	Asn	Ile	Leu	Leu		
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ggc	ctc	aag	ggc	ctg	gcc	cca	gct	gag	atc	tct	gca	gtg	tgt	gaa	aaa	487	
Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	Ile	Ser	Ala	Val	Cys	Glu	Lys		
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ggg	aat	ttc	aac	gtg	gcc	cat	ggg	ctg	gca	tgg	tca	tat	tac	atc	gga	535	
Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	Ala	Trp	Ser	Tyr	Tyr	Ile	Gly		
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Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln	Ala	Arg	Ile	Arg	Thr	Tyr		
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Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly	Ala	Val	Ser	Gln	Arg	Leu		
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Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val	Pro	Asp	Asn	Leu	Ser	Met		
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Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys	Leu	Pro	Gln	Gln	Thr	Gly		
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gac	cgt	gct	ggc	atc	aag	gat	cgg	gtt	tac	agc	aac	agc	atc	tat	gag	775	
Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr	Ser	Asn	Ser	Ile	Tyr	Glu		
	195					200					205						
ctt	ctg	gag	aac	ggg	cag	cgg	gcg	ggc	acc	tgt	gtc	ctg	gag	tac	gcc	823	
Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr	Cys	Val	Leu	Glu	Tyr	Ala		
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acc	ccc	ttg	cag	act	ttg	ttt	gcc	atg	tca	caa	tac	agt	caa	gct	ggc	871	
Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser	Gln	Tyr	Ser	Gln	Ala	Gly		
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ttt	agc	cgg	gag	gat	agg	ctt	gag	cag	gcc	aaa	ctc	ttc	tgc	cgg	aca	919	
Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala	Lys	Leu	Phe	Cys	Arg	Thr		
			245					250					255				
ctt	gag	gac	atc	ctg	gca	gat	gcc	cct	gag	tct	cag	aac	aac	tgc	cgc	967	
Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu	Ser	Gln	Asn	Asn	Cys	Arg		
		260					265						270				
ctc	att	gcc	tac	cag	gaa	cct	gca	gat	gac	agc	agc	ttc	tcg	ctg	tcc	1015	
Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp	Ser	Ser	Phe	Ser	Leu	Ser		
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cag	gag	gtt	ctc	cgg	cac	ctg	cgg	cag	gag	gaa	aag	gaa	gag	gtt	acc	1063	
Gln	Glu	Val	Leu	Arg	His	Leu	Arg	Gln	Glu	Glu	Lys	Glu	Glu	Val	Thr		
290					295					300					305		
gtg	ggc	agc	ttg	aag	acc	tca	gcg	gtg	ccc	agt	acc	tcc	acg	atg	tcc	1111	
Val	Gly	Ser	Leu	Lys	Thr	Ser	Ala	Val	Pro	Ser	Thr	Ser	Thr	Met	Ser		
				310					315					320			
caa	gag	cct	gag	ctc	ctc	ctc	agt	gga	atg	gga	aag	ccc	ctc	cct	ctc	1159	
Gln	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Gly	Met	Gly	Lys	Pro	Leu	Pro	Leu		
			325					330					335				
cgc	acg	gat	ttc	tct	tgag	acccag	ggc	caccagg	ccag	agcctc	cag	tggtctc				1214	

Arg Thr Asp Phe Ser

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340
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Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr Tyr
10                               15                               20                               25
cgc gac tgg ctg ctg cgg cgc gag gat gtt tta gaa gaa tgt atg tct 148
Arg Asp Trp Leu Leu Arg Arg Glu Asp Val Leu Glu Glu Cys Met Ser
                               30                               35                               40
ctt ccc aag cta tct tct tat tct gga tgg gtg gta gag cac gtc cta 196
Leu Pro Lys Leu Ser Ser Tyr Ser Gly Trp Val Val Glu His Val Leu
                               45                               50                               55
ccc cat atg cag gag aac caa cct ctg tct gag act tcg cca tcc tct 244
Pro His Met Gln Glu Asn Gln Pro Leu Ser Glu Thr Ser Pro Ser Ser
                               60                               65                               70
acg tca gct tca gcc cta gat caa ccc tca ttt gtt ccc aaa tct cct 292
Thr Ser Ala Ser Ala Leu Asp Gln Pro Ser Phe Val Pro Lys Ser Pro
                               75                               80                               85
gac gca agc tct gcc ttt tcc cca gcc tcc cct gca aca cca aat gga 340
Asp Ala Ser Ser Ala Phe Ser Pro Ala Ser Pro Ala Thr Pro Asn Gly
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acc aag ggc aaa aaa aaa aaa 361
Thr Lys Gly Lys Lys Lys Lys
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    1           5           10          15
agc tcc cta gaa tct cct gga atg ctt aat gga cct ttc cag cac cga      95
Ser Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg
           20           25           30
aat tca aga att atg act cat cgg tca gca gaa aag tgaggataacc      141
Asn Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
           35           40
ttttcctaac ctacctgctt cccctgcagt ttcttcacaa tcttactctt tatatttttag      201
catatgtagc ttctcaggat gttaattctg ttctctctgt gttggtgtct gagcaccag      261
aaggtagagc cagggggcact tataaaccag gagcattatt tgacaggcac ttaagaaaga      321
cactggctac gtaatccag cactttggga ggctgaggcg gatggatcac atgaggtcag      381
gagttcgaga ccagcctggc cagcatgggtg aaaccctgtc tctactaaaa atacaaaaat      441
tagctgggtg tggttgcaca cgctgtaat cccagctacc tgggaggctg aggcaggaga      501
atcgcttgaa cttgggaggc ggaggttgca gtgagcctag attttgccat tgcactccag      561
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score 3.7

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Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys
           -5           1           5
gag ccc act cag cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg      149
Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp
           10           15           20
aat aag aaa ggc aac gtt ttg cag ctt cca aat ttc tgaagaaact      195
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ttggctaccc	ggttcaattg	ctttttatctt	ttaatgtctt	gactcttcag	agttcgtacc							315
tcaaaagaac	aatgagaaca	tttgctttgc	tttctgctga	atccctaatac	tcaacaatct							375
atacctggac	tgtccagttc	tcctcctgtg	ctatctttctc	ttctatccaa	gtagaatgta							435
tgccaggagc	tccttccttc	tagcaatttc	tactaaaatg	tccaagtaga	atgtttcctt							495
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gatcctgggc aaagtttccc acgttgaggg tctcgaggac gcctagatct ctttcccagg	180
gcc atg gcg aac ccg aag ctg ctg gga ctg gag cta agc gag gcg gag	228
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu	
-15 -10 -5	
gcg atc ggt gct gat tcg gcg cga ttt gag gag ctg ctg ctg cag gcc	276
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala	
1 5 10	
tcg aag gag ctc cag caa gcc cag aca acc aga cca gaa tcg aca caa	324
Ser Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln	
15 20 25	
atc cag cct cag cct ggt ttc tgc ata aag acc aac tcc tcg gaa ggg	372
Ile Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly	
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aag gtt ttc atc aac atc tgc cac tcc ccc tct atc cct cct ccc gcc	420
Lys Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala	
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Asp Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala	
65 70 75	
ggg ttt cgc atc ccc atg agt ctg gga gag cct cat gca gaa ctg gat	516

Gly	Phe	Arg	Ile	Pro	Met	Ser	Leu	Gly	Glu	Pro	His	Ala	Glu	Leu	Asp	
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gca	aaa	ggc	cag	gga	tgt	acc	gcc	tac	gac	gta	gct	gtc	aac	agc	gac	564
Ala	Lys	Gly	Gln	Gly	Cys	Thr	Ala	Tyr	Asp	Val	Ala	Val	Asn	Ser	Asp	
	95				100					105						
ttc	tac	cgg	agg	atg	cag	aac	agc	gat	ttc	ttg	cgg	gag	ctc	gtg	atc	612
Phe	Tyr	Arg	Arg	Met	Gln	Asn	Ser	Asp	Phe	Leu	Arg	Glu	Leu	Val	Ile	
110				115					120					125		
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Thr	Ile	Ala	Arg	Glu	Gly	Leu	Glu	Asp	Ile	Tyr	Asn	Leu	Gln	Leu	Asn	
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ccg	gaa	tgg	cgc	atg	atg	aag	aac	cgg	cca	ttc	atg	ggc	tcc	atc	tcg	708
Pro	Glu	Trp	Arg	Met	Met	Lys	Asn	Arg	Pro	Phe	Met	Gly	Ser	Ile	Ser	
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Gln	Gln	Asn	Ile	Arg	Ser	Glu	Gln	Arg	Pro	Arg	Ile	Gln	Glu	Leu	Gly	
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Asp	Leu	Tyr	Thr	Pro	Ala	Pro	Gly	Arg	Ala	Glu	Ser	Gly	Pro	Glu	Lys	
	175				180						185					
cct	cac	ctg	aac	ctg	tgg	ctg	gaa	gcc	ccc	gac	ctc	ctc	ttg	gcc	gaa	852
Pro	His	Leu	Asn	Leu	Trp	Leu	Glu	Ala	Pro	Asp	Leu	Leu	Leu	Ala	Glu	
190			195					200						205		
gtt	gac	ctc	ccc	aaa	ctg	gat	gga	gcc	ctg	ggg	ctg	tcg	ctg	gag	atc	900
Val	Asp	Leu	Pro	Lys	Leu	Asp	Gly	Ala	Leu	Gly	Leu	Ser	Leu	Glu	Ile	
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Gly	Arg	Thr	Ala	Trp												
	225															
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Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
-30 -25 -20
act ggc tgg gca ggt att gct gtg ctt tac tta cat ctt tat gat gta 153
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
-15 -10 -5
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Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln
1 5 10
agt ctg aac tgc tta acc aag cgc tcc atc acc ttc ctt tgt ggg gat 249
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp
15 20 25 30
gca ggc ccc ctg gca gtg gcc gct gtg cta tat cat aag atg aac aat 297
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn
35 40 45
gag aag cag gca gaa gat tgc atc aca cgg cta att cac cta aat aag 345
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys
50 55 60
att gat cct cat gct cca aat gaa atg ctc tat ggg cga ata ggc tac 393
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr
65 70 75
atc tat gct ctt ctt ttt gtc aat aag aac ttt gga gtg gaa aag act 441
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr
80 85 90
cct caa agc cat att cag cag att tgt gaa aca att tta acc tct gga 489
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly
95 100 105 110
gaa aac cta gct agg aag aga aac ttc acg gca aag tct cca ctg atg 537
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met
115 120 125
tat gaa tgg tac cag gaa tat tat gta ggg gct gct cat ggc ctg gct 585
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
130 135 140
gga att tat tac tac ctg atg cag ccc agc ctt caa gtg agc caa ggg 633
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
145 150 155
aag tta cat agt ttg gtc aag ccc agt gta gac tac gtc tgc cag ctg 681
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
160 165 170
aaa ttc cct tct ggc aat tac cct cca tgt ata ggt gat aat cga gat 729
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
175 180 185 190
ctg ctt gtc cat tgg tgc cat ggc gcc cct ggg gta atc tac atg ctc 777
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
195 200 205
atc cag gcc tat aag gta ttc aga gag gaa aag tat ctc tgt gat gcc 825
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala
210 215 220
tat cag tgt gct gat gtg atc tgg caa tat ggg ttg ctg aag aag gga 873
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
225 230 235
tat ggg ctg tgc cac ggt tct gca ggg aat gcc tat gcc ttc ctg aca 921
Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
240 245 250

<222> 63..398

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<221> sig_peptide

<222> 63..206

<223> Von Heijne matrix

score 4.9

seq PSLAAGLLFGSLA/GL

<400> 97

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aa atg cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt      107
  Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe
      -45                      -40                      -35

ggc tac gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa      155
Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys
      -30                      -25                      -20

gca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta      203
Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
      -15                      -10                      -5

gcc ggc ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg      251
Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp
      1                      5                      10                      15

gtt ttc cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg      299
Val Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg
      20                      25                      30

ttc tac cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc      347
Phe Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala
      35                      40                      45

agt ttg ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc      395
Ser Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro
      50                      55                      60

cat tagcagaagt catgttccag cttagactga tgaagaatta aaaatctgca      448
His
tcttccacta ttttcaatat attaagagaa ataagtgcag catttttgca tctgacattt      508
tacctaaaaa aaaagacacc aaacttggca gagaggtgga aaatcagtca tgattacaaa      568
cctacagagg tggcgagtat gtaacacaag agctt      603
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<210> 98

<211> 522

<212> DNA

<213> Homo sapiens

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<222> 2..163

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<222> 488..493

<220>

<221> polyA_site

<222> 511..522

<220>

<221> misc_feature

<222> 164..165,305
 <223> n=a, g, c or t

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 Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
 1 5 10 15
 ccc cga tgg cac cga ttg cca ccg caa agc cta cag cac cac cag tat 97
 Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
 20 25 30
 tgc cag cgt cgc tgg cct gac cgc cgc tgc cta cag agt cac act caa 145
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
 35 40 45
 tcc tcc ggg cac ctt cct nntgaaggag tggctaagggt tggacaatac 193
 Ser Ser Gly His Leu Pro
 50
 acgttcactg cagctgctgt cggggccgtg tttggcctca ccacctgcat cagcgcccat 253
 gtccgcgaga agcccagca cccctgaac tacttccccg gtggctgcgc cnggaggcct 313
 gactctggga gcacgcacgc acaactacgg gattggcgcc gccgcctgcg tgtactttgg 373
 catagcggcc tccttggtca agatgggccc gctggagggc tgggaggtgt ttgcaaaacc 433
 caaggtgtga gccctgtgcc tgccgggacc tccagcctgc agaatgcgtc cagaaataaa 493
 ttctgtgtct gtgtgtgaaa aaaaaaaaaa 522

<210> 99
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 <212> DNA
 <213> Homo sapiens

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 <222> 13..465

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 <222> 13..75
 <223> Von Heijne matrix
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 seq PVAVTAAVAPVLS/IN

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 <222> 1,27,30,35,212,788,918,920..921
 <223> n=a, g, c or t

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 Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr
 -20 -15 -10
 gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg 99
 Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
 -5 1 5
 cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag 147
 Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
 10 15 20
 cgg ggc cta cta cac agt agc aaa tgg tcg gcg gag ttg gct ttc tct 195
 Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
 25 30 35 40

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ctc cct gca ttg cct cnt ggc cag ctg caa ccg cct ccg cct att aca      243
Leu Pro Ala Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr
          45          50          55
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac      291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
          60          65          70
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc      339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
          75          80          85
aat agc aag aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg      387
Asn Ser Lys Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
          90          95          100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
          105          110          115          120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
          125          130
gaatgaatgt actttataca tagcaataat aaaaaaaga tatcataaat aaagttaaaa      545
aggatggtag agaagaaaat attcttagga atgactaaca ggataagtaa caacctgatt      605
atattatttac tttaggttat ataaggttct tcatgcctgt gaattaatat tattgtgtaa      665
gaattaagtt aaaaagcctg ggctgacttt taaatttata aattcattta tcatgtttat      725
agtatattta ttgttttctt ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca      785
agnaaaccaa cttaatactg tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tactttccta ctttttctta gttgttatct atataaattg attaaaaaaa      905
cattttatgt acntnncatt tcctagtaca ggttgagtat cccttatttg a          956

<210> 100
<211> 1041
<212> DNA
<213> Homo sapiens

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<222> 20..703

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<221> sig_peptide
<222> 20..94
<223> Von Heijne matrix
      score 3.9
      seq ATVGLLLMLGVTLP/NS

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<222> 1000..1005

<220>
<221> polyA_site
<222> 1023..1041

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          Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe
          -25          -20          -15
atg gca act gtg ggg ctg ctg atg ctg ggg gtg act ctg cca aac agc      100
Met Ala Thr Val Gly Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser

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tac tgg cga gtg tcc act gtg cac ggg aac gtc atc acc acc aac acc				148
Tyr Trp Arg Val Ser Thr Val His Gly Asn Val Ile Thr Thr Asn Thr				
5 10 15				
atc ttc gag aac ctc tgg ttt agc tgt gcc acc gac tcc ctg ggc gtc				196
Ile Phe Glu Asn Leu Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val				
20 25 30				
tac aac tgc tgg gag ttc ccg tcc atg ctg gcc ctc tct ggg tat att				244
Tyr Asn Cys Trp Glu Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile				
35 40 45 50				
cag gcc tgc cgg gca ctc atg atc acc gcc atc ctc ctg ggc ttc ctc				292
Gln Ala Cys Arg Ala Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu				
55 60 65				
ggc ctc ttg cta ggc ata gcg ggc ctg cgc tgc acc aac att ggg ggc				340
Gly Leu Leu Leu Gly Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly				
70 75 80				
ctg gag ctc tcc agg aaa gcc aag ctg gcg gcc acc gca ggg gcc ccc				388
Leu Glu Leu Ser Arg Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro				
85 90 95				
cac att ctg gcc ggt atc tgc ggg atg gtg gcc atc tcc tgg tac gcc				436
His Ile Leu Ala Gly Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala				
100 105 110				
ttc aac atc acc cgg gac ttc ttc gac ccc ttg tac ccc gga acc aag				484
Phe Asn Ile Thr Arg Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys				
115 120 125 130				
tac gag ctg ggc ccc gcc ctc tac ctg ggg tgg agc gcc tca ctg atc				532
Tyr Glu Leu Gly Pro Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile				
135 140 145				
tcc atc ctg ggt ggc ctc tgc ctc tgc tcc gcc tgc tgc tgc ggc tct				580
Ser Ile Leu Gly Gly Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser				
150 155 160				
gac gag gac cca gcc gcc agc gcc cgg cgg ccc tac cag gct cca gtg				628
Asp Glu Asp Pro Ala Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val				
165 170 175				
tcc gtg atg ccc gtc gcc acc tgc gac caa gaa ggc gac agc agc ttt				676
Ser Val Met Pro Val Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe				
180 185 190				
ggc aaa tac ggc aga aac gcc tac gtg tagcagctct ggcccgtggg				723
Gly Lys Tyr Gly Arg Asn Ala Tyr Val				
195 200				
ccccgtgtgc ttccactgc cccaaggaga ggggacctgg ccgggggcca ttccctata				783
gtaacctcag gggccggcca cgcccgcgc ccgtagcccc gcccggcca cggccccgtg				843
tcttgactgc tcatggcccc tccaggccaa gaactgctct tgggaagtgc catatctccc				903
ctctgaggct ggatccctca tcttctgacc ctgggttctg ggctgtgaag gggacggtgt				963
ccccgcacgt ttgtattgtg tataaatata ttcattaata aatgcatatt gtgaccgtta				1023
aaaaaaaaa aaaaaaaaa				1041

<210> 101
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 <213> Homo sapiens

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 <221> CDS
 <222> 103..294

<220>


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<221> sig_peptide
<222> 103..243
<223> Von Heijne matrix
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      seq TWLGLLSFQNLHC/FP

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taacattaac ttccttaagt aataatcaat gaaagaaatt ct atg cat ggt ttt      114
                               Met His Gly Phe
                               -45
gaa ata ata tcc ttg aaa gag gaa tca cca tta gga aag gtg agt cag      162
Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly Lys Val Ser Gln
      -40                               -35                               -30
ggt cct ttg ttt aat gtg act agt ggc tca tca tca cca gtg acc tgg      210
Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser Pro Val Thr Trp
      -25                               -20                               -15
ttg ggc cta ctc tcc ttc cag aac ctg cat tgc ttc cca gac ctc ccc      258
Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe Pro Asp Leu Pro
      -10                               -5                               1                               5
act gag atg cct cta aga gcc aaa gga gtc aac act tgagcctagg      304
Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
      10                               15
gtgggctaca acaaaagatt ctaatttacc ttgcttcac taggtccagg cccaagtag      364
cttgctgaag gaacttaaaa agtagctgtt atttattgta ttgtataagc taaaaacatt      424
tatttttgtt gaatcgaaac aattccatgt agcaatcttt tttctgttca cgggtgttgt      484
gatagaacct taaattccgc aagcatcagt tttttgaaaa aatgggaatt gaccggatag      544
taacaggcaa agtt      558

<210> 102
<211> 730
<212> DNA
<213> Homo sapiens

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<222> 81..518

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<222> 81..173
<223> Von Heijne matrix
      score 3.9
      seq ILFHGVFYAGGFA/IV

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attttcaaga gagttgtgct atg atg tgg caa aag tat gca gga agc agg cgg      113
                               Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg
                               -30                               -25
tca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc      161
Ser Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
      -20                               -15                               -10                               -5
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg      209
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
      1                               5                               10
gct tta tat tac aag ttg gca gtg gag cag ctg cag agc cat ccc gag      257

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Ala	Leu	Tyr	Tyr	Lys	Leu	Ala	Val	Glu	Gln	Leu	Gln	Ser	His	Pro	Glu		
	15						20					25					
gca	cag	gaa	gct	ctg	ggc	cct	cct	ctc	aac	atc	cat	tat	ctc	aag	ctc		305
Ala	Gln	Glu	Ala	Leu	Gly	Pro	Pro	Leu	Asn	Ile	His	Tyr	Leu	Lys	Leu		
	30					35					40						
atc	gac	agg	gaa	aac	ttc	gtg	gac	att	gtt	gat	gcc	aag	ttg	aag	att		353
Ile	Asp	Arg	Glu	Asn	Phe	Val	Asp	Ile	Val	Asp	Ala	Lys	Leu	Lys	Ile		
45				50					55				60				
cct	gtc	tct	gga	tcc	aaa	tca	gag	ggc	ctt	ctc	tac	gtc	cac	tca	tcc		401
Pro	Val	Ser	Gly	Ser	Lys	Ser	Glu	Gly	Leu	Leu	Tyr	Val	His	Ser	Ser		
			65				70				75						
aga	ggt	ggc	ccc	ttt	cag	agg	tgg	cac	ctt	gac	gag	gtc	ttt	tta	gag		449
Arg	Gly	Gly	Pro	Phe	Gln	Arg	Trp	His	Leu	Asp	Glu	Val	Phe	Leu	Glu		
			80				85				90						
ctc	aag	gat	ggt	cag	cag	att	cct	gtg	ttc	aag	ctc	agt	ggg	gaa	aac		497
Leu	Lys	Asp	Gly	Gln	Gln	Ile	Pro	Val	Phe	Lys	Leu	Ser	Gly	Glu	Asn		
	95					100					105						
ggt	gat	gaa	gtg	aaa	aag	gag	tagagacgac	ccagaagacc	cagcttgctt								548
Gly	Asp	Glu	Val	Lys	Lys	Glu											
	110					115											
ctagtccatc	cttccctcat	ctctaccata	tggtccactgg	ggtggtggcc	catctcagtg												608
acagacactc	ctgcaaccca	gttttccagc	caccagtggg	atgatggtat	gtgccagcac												668
atggttaattt	tggtgtaatt	ctaacttggg	cacaacgaat	gctatttgtc	atttttaaac												728
tg																	730

<210> 103
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 <212> DNA
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 <222> 66..326

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 <222> 1066..1071

<220>
 <221> polyA_site
 <222> 1087..1098

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	Met	Glu	Leu	Ala	Pro	Thr	Ala	Arg	Leu	Pro	Pro	Gly	His	Gly	Ser		
	1			5					10				15				
ttg	ccc	cat	ggt	gtc	ctg	gga	ccc	aga	gca	aca	gga	tct	gtc	acc	cac		158
Leu	Pro	His	Gly	Val	Leu	Gly	Pro	Arg	Ala	Thr	Gly	Ser	Val	Thr	His		
				20				25				30					
ctc	tct	ctt	ctc	ccc	cag	atc	aag	caa	cgt	gcc	tca	gag	gct	ttg	ccc		206
Leu	Ser	Leu	Leu	Pro	Gln	Ile	Lys	Gln	Arg	Ala	Ser	Glu	Ala	Leu	Pro		
			35				40				45						
gaa	ttg	ctt	cgt	cct	gtc	acc	ccc	atc	acc	aat	ttt	gag	ggc	agc	cag		254
Glu	Leu	Leu	Arg	Pro	Val	Thr	Pro	Ile	Thr	Asn	Phe	Glu	Gly	Ser	Gln		
	50					55					60						
tct	cag	gac	cac	agt	gga	atc	ttt	ggc	ctg	gta	aca	aac	ctg	gaa	gag		302

Ser	Gln	Asp	His	Ser	Gly	Ile	Phe	Gly	Leu	Val	Thr	Asn	Leu	Glu	Glu	
65					70					75						
ctg	gag	gtg	gac	gat	tgg	gag	ttc	tgagcctctg	caaactgtgc	gcattctcca						356
Leu	Glu	Val	Asp	Asp	Trp	Glu	Phe									
80					85											
gccaggggatg	cagaggccac	ccagaggccc	ttcctgaggg	cgggccacat	tcccgccttc											416
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aagaaaatcc	tgagagata	cttcactgct	ccaaggcttt	tgagacacaa	gggaatctca											536
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tcctccgcag	aagagagatg	ctgctctggc	cctgggagct	gaattccaag	cccagggttt											656
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ttaactttgc	tctcagatgc	ctcagatgct	ataggtcagt	gaaagggcga	gtagtaagct											776
gcctgcctcc	cttccctcag	acctctccct	cataattcca	gagaagggca	tttctgtctt											836
tttaagcaca	gactaaggct	ggaacagtcc	atccttatcc	ctcttctggc	ttgggacctg											896
acacctaagt	ctttcccacg	gtttatgtgt	gtgcctcatt	cctttcccac	caagaatcca											956
tcttagcgcc	tcctgccagc	tgccctgggtg	ctttctccaa	gggccatcag	tgtcttgctt											1016
agcttgaggg	cttaagtcct	tatgctgtgt	tagtttcgtt	gtcagaacaa	attaaaattt											1076
tcagagacgc	aaaaaaaaaa	aa														1098

<210> 104
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 <213> Homo sapiens

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 <222> 170..289

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 <222> 170..250
 <223> Von Heijne matrix
 score 3.6
 seq LLLLLITPSPSPL/LF

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agtctgcatt	acacaaatag	acactaattt	atttgaaca	agcagcaaa	atg aga act											178
					Met Arg Thr											
					-25											

tta	ttt	ggt	gca	gtc	agg	gct	cca	ttt	agt	tcc	ctc	act	ctg	ctt	cta	226
Leu	Phe	Gly	Ala	Val	Arg	Ala	Pro	Phe	Ser	Ser	Leu	Thr	Leu	Leu	Leu	
			-20				-15				-10					
atc	acc	cct	tct	ccc	agc	cct	ctt	cta	ttt	gat	aga	ggt	ctg	tcc	ctc	274
Ile	Thr	Pro	Ser	Pro	Ser	Pro	Leu	Leu	Phe	Asp	Arg	Gly	Leu	Ser	Leu	
		-5				1					5					
aga	tca	gca	atg	tct	tagccctctt	cctctcttcc	attccttctt	gttggtactc								329
Arg	Ser	Ala	Met	Ser												
		10														
atttcttcta	acttttta															346

<210> 105
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 <212> DNA
 <213> Homo sapiens

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<222> 18..320
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 <222> 539..544

<220>
 <221> polyA_site
 <222> 542..554

<220>
 <221> misc_feature
 <222> 278
 <223> n=a, g, c or t

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 Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly
 1 5 10
 act gtt atc act cca gat aca tgg aaa gat ggt gct agg aat acc aca 98
 Thr Val Ile Thr Pro Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr
 15 20 25
 gaa agt ggt gga aga aag ctg aat aaa aat aaa gct ttg act tca aaa 146
 Glu Ser Gly Gly Arg Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys
 30 35 40
 aaa gca aga ttt gat cca tat gga aag aat aag ttc tcc act tgt aga 194
 Lys Ala Arg Phe Asp Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg
 45 50 55
 att tgt aaa agt tct gtg cac caa cca ggt tct cat tac tgc cag ggc 242
 Ile Cys Lys Ser Ser Val His Gln Pro Gly Ser His Tyr Cys Gln Gly
 60 65 70 75
 tgt gcc tac aaa aaa ggc atc tgt gcg atg tgt ggn aaa aaa gtt ttg 290
 Cys Ala Tyr Lys Lys Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu
 80 85 90
 gat acc aaa aac tac aag caa aca tct gtc tagatgtatt gatggaattt 340
 Asp Thr Lys Asn Tyr Lys Gln Thr Ser Val
 95 100
 ctggctttct aaatgatttt actttctgcc ttgaattttc aaggcataga tgtcaactta 400
 cagaataaca tgttttaaga taattaagtt taaaccagag aatttgattg ttactcattt 460
 tgctctcatg ttctaaacag caacagtgtg actagtcttt tggtgtaa at gggtattttt 520
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 cccgaccctc atg ttc gaa gag cct gag tgg gcc gag gcg gcc cca gta 109
 Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val
 -20 -15 -10
 gcc gcg ggc ctt ggg ccc gta atc tca cga cct ccg cct gcg gcc tcc 157
 Ala Ala Gly Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser
 -5 1 5
 tcg caa aac aag ggc tcc aag cgc cgc cag ctc ttg gcc aca tta cgg 205
 Ser Gln Asn Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg
 10 15 20
 gcc cta gag gca gca tct ctt tcc cag cat ccc ccc agc cta tgt ata 253
 Ala Leu Glu Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile
 25 30 35
 agt gac tct gag gag gag gag gag gaa agg aag aaa tgc ccc aaa 301
 Ser Asp Ser Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys
 40 45 50 55
 aag gca tca ttt gcc agt gcc tct gct gaa gta ggg aag aaa ggg aag 349
 Lys Ala Ser Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys
 60 65 70
 aag aaa tgt caa aaa cag ggc cca cct tgc agt gac tct gag gaa gaa 397
 Lys Lys Cys Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Glu
 75 80 85
 gta gaa agg aag aag aaa tgc cac aaa cag gct ctt gtt ggc agt gac 445
 Val Glu Arg Lys Lys Lys Cys His Lys Gln Ala Leu Val Gly Ser Asp
 90 95 100
 tct gct gaa gat gag aaa aga aag agg aaa tgc cag aaa cat gcc cct 493
 Ser Ala Glu Asp Glu Lys Arg Lys Arg Lys Cys Gln Lys His Ala Pro
 105 110 115
 ata aat tca gcc cag cac ctg gac aat gtt gac caa aca ggt ccc aaa 541
 Ile Asn Ser Ala Gln His Leu Asp Asn Val Asp Gln Thr Gly Pro Lys
 120 125 130 135
 gcc tgg aag ggt agt act aca aat gat cca cca aag caa agc cct ggg 589
 Ala Trp Lys Gly Ser Thr Thr Asn Asp Pro Pro Lys Gln Ser Pro Gly
 140 145 150
 tcc act tcc cct aaa ccc cct cat aca tta agc cgc aag cag tgg cgg 637
 Ser Thr Ser Pro Lys Pro Pro His Thr Leu Ser Arg Lys Gln Trp Arg
 155 160 165
 aac cgg caa aag aat aag aga aga tgt aag aac aag ttt cag cca cct 685
 Asn Arg Gln Lys Asn Lys Arg Arg Cys Lys Asn Lys Phe Gln Pro Pro
 170 175 180
 cag gtg cca gac cag gcc cca gct gag gcc ccc aca gag aag aca gag 733
 Gln Val Pro Asp Gln Ala Pro Ala Glu Ala Pro Thr Glu Lys Thr Glu
 185 190 195
 gtg tct cct gtt ccc agg aca gac agc cat ggg gct cgg gca ggg gct 781
 Val Ser Pro Val Pro Arg Thr Asp Ser His Gly Ala Arg Ala Gly Ala
 200 205 210 215
 ttg cga gcc cgc atg gca cag cgg ctg gat ggg gcc cga ttt cgc tac 829
 Leu Arg Ala Arg Met Ala Gln Arg Leu Asp Gly Ala Arg Phe Arg Tyr

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ctc aat gaa cag ttg tac tca ggg ccc agc agt gct gca cag cgt ctc				877
Leu Asn Glu Gln Leu Tyr Ser Gly Pro Ser Ser Ala Ala Gln Arg Leu				
	235	240	245	
ttc cag gaa gac cct gag gct ttt ctt ctc tac cac cgc ggc ttc cag				925
Phe Gln Glu Asp Pro Glu Ala Phe Leu Leu Tyr His Arg Gly Phe Gln				
	250	255	260	
agc caa gtg aag aag tgg cca ctg cag cca gtg gac cgc atc gcc agg				973
Ser Gln Val Lys Lys Trp Pro Leu Gln Pro Val Asp Arg Ile Ala Arg				
	265	270	275	
gat ctt cgc cag cgg cct gca tcc cta gtg gtg gct gac ttc ggc tgt				1021
Asp Leu Arg Gln Arg Pro Ala Ser Leu Val Val Ala Asp Phe Gly Cys				
	280	285	290	295
ggg gat tgc cgc ttg gct tca agt atc cgg aac cct gtg cat tgc ttt				1069
Gly Asp Cys Arg Leu Ala Ser Ser Ile Arg Asn Pro Val His Cys Phe				
	300	305	310	
gac ttg gct tct ctg gac cct agg gtc act gtg tgt gac atg gcc cag				1117
Asp Leu Ala Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln				
	315	320	325	
gtt cct ttg gag gat gag tct gtg gat gtg gct gtg ttt tgc ctt tca				1165
Val Pro Leu Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser				
	330	335	340	
ctg atg gga acc aac atc agg gac ttc cta gag gag gca aat aga gta				1213
Leu Met Gly Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val				
	345	350	355	
ctg aag cca ggg ggt ctc ctg aaa gtg gct gag gtc agc agc cgc ttt				1261
Leu Lys Pro Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe				
	360	365	370	375
gag gat gtt cga acc ttt ctg cgg gct gtg acc aag cta ggc ttc aag				1309
Glu Asp Val Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys				
	380	385	390	
att gtc tcc aag gac ctg acc aac agc cat ttc ttc ttg ttt gat ttc				1357
Ile Val Ser Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe				
	395	400	405	
caa aag act ggg ccc cct ctg gta ggg ccc aag gct cag ctt tca ggc				1405
Gln Lys Thr Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly				
	410	415	420	
ctg cag ctt cag cca tgt ctc tac aag cgc agg tgacctctgg atcttccttg				1458
Leu Gln Leu Gln Pro Cys Leu Tyr Lys Arg Arg				
	425	430		
agaggggagg cagatctcaa actccaggct cagaactgtg aagactgttt ccggcctggc				1518
tgtgagccaa gacctggttc ctggtggacc ctgaggacaa agtgtgataa aacctctggc				1578
tcagacttgc tctactgaag gcttcttggt tataagatgc ataaagtcac tggggctagc				1638
taaacaataa agagtttatt gtgaggaaaa aaaaaaaaaa				1678

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 <222> 25..75


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<222> 520
<223> n=a, g, c or t

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tacccttgag tgatgtgcct tga atg acg ctg ctt tca ttc gct gct ttc acg      113
                Met Thr Leu Leu Ser Phe Ala Ala Phe Thr
                        -25                        -20

gct gct ttc tcc gtc ctc ccc tgt tac tac ctt ggg ctg ttt cag cgg      161
Ala Ala Phe Ser Val Leu Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg
                -15                -10                -5

gcg ctc gcg tcg gtc ttc gac cca ctt tgc gtt tgt tca cgt gtg ctc      209
Ala Leu Ala Ser Val Phe Asp Pro Leu Cys Val Cys Ser Arg Val Leu
                1                5                10

ccg aca cct gta tgt acc ttg gtc gca aca caa gcc gaa aaa ata tta      257
Pro Thr Pro Val Cys Thr Leu Val Ala Thr Gln Ala Glu Lys Ile Leu
    15                20                25

gag aat ggg ccc tgt cca acc aag gag gcg gcc cag ctt gtc ggg aag      305
Glu Asn Gly Pro Cys Pro Thr Lys Glu Ala Ala Gln Leu Val Gly Lys
    30                35                40                45

ggc agc gtt tcc gcc aga aat gct tcg tgaaaggcac ttgagggacc      352
Gly Ser Val Ser Ala Arg Asn Ala Ser
                50

ttagcagcat cctcaacagg ccttgtaggg aatgccagaa gaagcagtc ttggccgggc      412
ggggtggctc atgcctgtgg tcccagcact ttgggaggcc ggggcgggcg gatcacctga      472
ggtcgggagg tccagaccag cctgaccgac atggagaaac cccgtctnta ctagaaatac      532
aaaactagcc ggggtgtggtg gcgcatgcct gtagtcccag ctactcggga gggtgaggca      592
ggagacgttc ttgaaccgag gaggcggagt ttgtggtgag ccgagatcgc gccattgcac      652
tccagcctgg gcatgccaaag agcgaaactc cgtctcaaaa aaaaaaaaga aaaaaaaaaa      712
aa                                                                    714

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<213> Homo sapiens

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<222> 32..100
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<222> 770..775

<220>
<221> polyA_site
<222> 793..805

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ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg cct 100
Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro
-15 -10 -5
ggg gcg gcc ggc ttc aca cct tcc ctg gat agc gac ttc acc ttt acc 148
Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr
1 5 10 15
ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg aag 196
Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys
20 25 30
gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta gat 244
Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp
35 40 45
att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt gaa 292
Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu
50 55 60
caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt gat 340
Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp
65 70 75 80
tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag gtg 388
Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val
85 90 95
att ttc ttt gaa tta atc ctg gat aat atg gga gaa cag gca caa gaa 436
Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu
100 105 110
caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat atg 484
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp Met
115 120 125
aaa ctg gaa gac atc ctg gaa tcc atc agc agc atc aag tcc aga cta 532
Lys Leu Glu Asp Ile Leu Glu Ser Ile Ser Ser Ile Lys Ser Arg Leu
130 135 140
agc aaa agt ggg cac ata caa att ctg ctt aga gca ttt gaa gct cgt 580
Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe Glu Ala Arg
145 150 155 160
gat cga aac ata caa gaa agc aac ttt gat aga gtc aat ttc tgg tct 628
Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val Asn Phe Trp Ser
165 170 175
atg gtt aat tta gtg gtc atg gtg gtg gtg tca gcc att caa gtt tat 676
Met Val Asn Leu Val Val Met Val Val Val Ser Ala Ile Gln Val Tyr
180 185 190
atg ctg aag agt ctg ttt gaa gat aag agg aaa agt aga act 718
Met Leu Lys Ser Leu Phe Glu Asp Lys Arg Lys Ser Arg Thr
195 200 205
taaaactcca aactagagta cgtaacattg aaaaatgagg cataaaaatg caataaactg 778
ttacagtcaa gaccaaaaaa aaaaaaa 805

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<222> 26..481

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<222> 26..88

<223> Von Heijne matrix

score 4.4

seq AVASSFFCASLFS/AV

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<222> 755..760

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<221> polyA_site

<222> 775..787

<400> 111

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-20 -15	
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Val Ala Ser Ser Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys	
-10 -5 1	
ata gaa gag gga cat att ggg gta tat tac aga ggc ggt gcc ctg ctg	148
Ile Glu Glu Gly His Ile Gly Val Tyr Tyr Arg Gly Gly Ala Leu Leu	
5 10 15 20	
act tcg acc agc ggc cct ggt ttc cat ctc atg ctc cct ttc atc aca	196
Thr Ser Thr Ser Gly Pro Gly Phe His Leu Met Leu Pro Phe Ile Thr	
25 30 35	
tca tat aag tct gtg cag acc aca ctc cag aca gat gag gtg aag aat	244
Ser Tyr Lys Ser Val Gln Thr Thr Leu Gln Thr Asp Glu Val Lys Asn	
40 45 50	
gta cct tgt ggg act agt ggt ggt gtg atg atc tac ttt gac aga att	292
Val Pro Cys Gly Thr Ser Gly Gly Val Met Ile Tyr Phe Asp Arg Ile	
55 60 65	
gaa gtg gtg aac ttc ctg gtc ccg aac gca gtg cat gat ata gtg aag	340
Glu Val Val Asn Phe Leu Val Pro Asn Ala Val His Asp Ile Val Lys	
70 75 80	
aac tat act gct gac tat gac aag gcc ctc atc ttc aac aag atc cac	388
Asn Tyr Thr Ala Asp Tyr Asp Lys Ala Leu Ile Phe Asn Lys Ile His	
85 90 95 100	
cac gaa ctg aac cag ttc tgc agt gtg cac acg ctt caa gag gtc tac	436
His Glu Leu Asn Gln Phe Cys Ser Val His Thr Leu Gln Glu Val Tyr	
105 110 115	
att gag ctg ttt gga ctg gaa aat gat ttt tcc cag gaa tct tca	481
Ile Glu Leu Phe Gly Leu Glu Asn Asp Phe Ser Gln Glu Ser Ser	
120 125 130	
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cagcaatcat aattaagcaa accgcctttt gcaccattta agatttagga aatcatccaa	601
attactttta atgtttctgc agtagaaaat gaatctaaat tcattttata gggtttgtag	661
tcttttatct gttttggatt cactgtgctt ttaagaaaaa gtttggtaaat ttgccgttga	721
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aaaaaa	787

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<212> DNA
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<222> 26..187
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score 4.1
seq AVVAAAARTGSEA/RV

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tct tcg ccg tct ttg aaa aca gac aca tcc cct gtc ctt gaa act gca 100
Ser Ser Pro Ser Leu Lys Thr Asp Thr Ser Pro Val Leu Glu Thr Ala
-45 -40 -35 -30
gga acg gtc gca gca atg gct gcg acc ccg tca gca agg gct gca gcc 148
Gly Thr Val Ala Ala Met Ala Ala Thr Pro Ser Ala Arg Ala Ala Ala
-25 -20 -15
gcg gtg gtt gcg gcc gcg gcc agg acc gga tcc gaa gcc agg gtc tcc 196
Ala Val Val Ala Ala Ala Ala Arg Thr Gly Ser Glu Ala Arg Val Ser
-10 -5 1
aag gcc gct ttg gct acc aag ctg ctg tcc ttg agc ggc gtg ttc gcc 244
Lys Ala Ala Leu Ala Thr Lys Leu Leu Ser Leu Ser Gly Val Phe Ala
5 10 15
gtg cac aag ccc aaa ggg ccc act tca gcc gag ctg ctg aat cgg ttg 292
Val His Lys Pro Lys Gly Pro Thr Ser Ala Glu Leu Leu Asn Arg Leu
20 25 30 35
aag gag aag ctg ctg gca gaa gct gga atg cct tct cca gaa tgg acc 340
Lys Glu Lys Leu Leu Ala Glu Ala Gly Met Pro Ser Pro Glu Trp Thr
40 45 50
aag agg aaa aag cag act ttg aaa att ggg cat gga ggg act cta gac 388
Lys Arg Lys Lys Gln Thr Leu Lys Ile Gly His Gly Gly Thr Leu Asp
55 60 65
agc gca gcc cga gga gtt ctg gtt gtt gga att gga agc gga aca aaa 436
Ser Ala Ala Arg Gly Val Leu Val Val Gly Ile Gly Ser Gly Thr Lys
70 75 80
atg ttg acc agt atg ttg tca ggg tcc aag agg tat act gcc att gga 484
Met Leu Thr Ser Met Leu Ser Gly Ser Lys Arg Tyr Thr Ala Ile Gly
85 90 95
gaa ctg ggg aaa gct act gat aca cta gat tct acg ggg aag gta aca 532
Glu Leu Gly Lys Ala Thr Asp Thr Leu Asp Ser Thr Gly Lys Val Thr
100 105 110 115
gaa gaa aaa cct tac ggt atg aac ctc atc taagtag 569
Glu Glu Lys Pro Tyr Gly Met Asn Leu Ile
120 125

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<212> DNA
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 <221> sig_peptide
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 score 6.8
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 <222> 858..863

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 <222> 881..893

<400> 113

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ctg ctt gaa gag ctt ccc ctc ccc gac cag cag cca tgc atc gag cct	96
Leu Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro	
-75 -70 -65	
cca cct tcc tcc atc atg tac cag gct aac ttt gac aca aac ttt gag	144
Pro Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu	
-60 -55 -50	
gac agg aat gca ttt gtc acg ggc att gca agg tac att gag cag gct	192
Asp Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala	
-45 -40 -35 -30	
aca gtc cac tcc agc atg aat gag atg ctg gag gaa gga cat gag tat	240
Thr Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr	
-25 -20 -15	
gcg gtc atg ctg tac acc tgg cgc agc tgt tcc cgg gcc att ccc cag	288
Ala Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln	
-10 -5 1	
gtg aaa tgc aac gag cag ccc aac cga gta gag atc tat gag aag aca	336
Val Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr	
5 10 15	
gta gag gtg ctg gag ccg gag gtc acc aag ctc atg aag ttc atg tat	384
Val Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr	
20 25 30 35	
ttt cag cgc aag gcc atc gag cgg ttc tgc agc gag gtg aag cgg ctg	432
Phe Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu	
40 45 50	
tgc cat gcc gag cgc agg aag gac ttt gtc tct gag gcc tac ctc ctg	480
Cys His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu	
55 60 65	
acc ctt ggc aag ttc atc aac atg ttt gct gtc ctg gat gag cta aag	528
Thr Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys	
70 75 80	
aac atg aag tgc agc gtc aag aat gac cac tcc gcc tac aag agg gca	576
Asn Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala	
85 90 95	
gca cag ttc ctg cgg aag atg gca gat ccc cag tct atc cag gag tcg	624

Arg	Gly	Lys	Gln	Cys	Leu	Asp	Phe	Thr	Val	Thr	Val	His	Phe	Phe	His	
45						50					55					
ctc	ctg	ggc	tgc	tgg	ttc	tac	agc	tcc	cgt	ttc	ccc	tcg	gcg	ctg	acc	345
Leu	Leu	Gly	Cys	Trp	Phe	Tyr	Ser	Ser	Arg	Phe	Pro	Ser	Ala	Leu	Thr	
60					65				70					75		
tgg	tgg	ctg	gtc	caa	gcc	gtg	tgc	att	gca	ctc	atg	gct	gtc	atc	ggg	393
Trp	Trp	Leu	Val	Gln	Ala	Val	Cys	Ile	Ala	Leu	Met	Ala	Val	Ile	Gly	
				80				85					90			
gag	tac	ctg	tgc	atg	cgg	acg	gag	ctc	aag	gag	ata	ccc	ctc	aac	tca	441
Glu	Tyr	Leu	Cys	Met	Arg	Thr	Glu	Leu	Lys	Glu	Ile	Pro	Leu	Asn	Ser	
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gcc	cct	aaa	tcc	aat	gtc	tagaatcagg	ccctttggac	atcccgtga								489
Ala	Pro	Lys	Ser	Asn	Val											
				110												
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atgccactct	tgagccacaa	tacctgtcac	cagcctgttg	ttttaagaga	gaaaaaaaaat											789
caaggatata	tgattggagc	aaaccacttc	tttagtcac	tgtcttacct	ccctgggaca											849
gctgttacct	ttgcagtgtt	gccgaatcac	agcagttacc	tttgcaatgt	tgccgaatca											909
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gtcttctagg	aatgaccagg	caccagctc	ccactggact	ccaatttttt	ttcctgcctt											1269
atttagaatt	ctttggcggg	aagggtatga	tgggttccca	gagacaagaa	gccaacctt											1329
ctggcctggg	ctgtgctgat	agtgtgagg	gagataggaa	tttgctgcta	agatttttct											1389
ttggggtgga	gtttcctctg	tgaggggctt	gcagctatcc	ttcctgtgta	tacaaataca											1449
gtattttcca	tgaaaaaaaa	aaaaaa														1475

<210> 115
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..248

<220>
 <221> sig_peptide
 <222> 48..161
 <223> Von Heijne matrix
 score 6.3
 seq LVFALVTAVCCLA/DG

<220>
 <221> polyA_signal
 <222> 283..288

<220>
 <221> polyA_site
 <222> 308..321

<400> 115

gctgagaaga gttgagggaa agtgctgctg ctgggtctgc agacgcg atg aat aac	56
	Met Asn Asn
gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc	104
Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly	
-35 -30 -25 -20	
cac gtg aag atg ctg cgg ctg gtg ttt gca ctt gtg aca gca gta tgc	152
His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr Ala Val Cys	
-15 -10 -5	
tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc	200
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro	
1 5 10	
aac ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg	248
Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu	
15 20 25	
tgattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca	308
aaaaaaaaaa aaa	321

<210> 116
 <211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..399

<220>
 <221> sig_peptide
 <222> 25..186
 <223> Von Heijne matrix
 score 3.5
 seq SILAQVLDQSARA/RL

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ctgctccagc gctgacgccg agcc atg gcg gac gag gag ctt gag gcg ctg	51
	Met Ala Asp Glu Leu Glu Ala Leu
	-50
agg aga cag agg ctg gcc gag ctg cag gcc aaa cac ggg gat cct ggt	99
Arg Arg Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly	
-45 -40 -35 -30	
gat gcg gcc caa cag gaa gca aag cac agg gaa gca gaa atg aga aac	147
Asp Ala Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn	
-25 -20 -15	
agt atc tta gcc caa gtt ctg gat cag tcg gcc cgg gcc agg tta agt	195
Ser Ile Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser	
-10 -5 1	
aac tta gca ctt gta aag cct gaa aaa act aaa gca gta gag aat tac	243
Asn Leu Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr	
5 10 15	
ctt ata cag atg gca aga tat gga caa cta agt gag aag gta tca gaa	291
Leu Ile Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu	
20 25 30 35	
caa ggt tta ata gaa atc ctt aaa aaa gta agc caa caa aca gaa aag	339
Gln Gly Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys	
40 45 50	
aca aca aca gtg aaa ttc aac aga aga aaa gta atg gac tct gat gaa	387
Thr Thr Thr Val Lys Phe Asn Arg Arg Lys Val Met Asp Ser Asp Glu	


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      55              60              65
gat gac gat tat tgaactacaa gtgctcacag actagaactt aacggaacaa      439
Asp Asp Asp Tyr
      70
gtctaggaca g      450

<210> 117
<211> 1173
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..1137

<220>
<221> sig_peptide
<222> 10..72
<223> Von Heijne matrix
      score 6.5
      seq LLTLLLPPPPPLYT/RH

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<221> polyA_signal
<222> 1144..1149

<220>
<221> polyA_site
<222> 1162..1173

<400> 117
gagctgctt atg gga cac cgc ttc ctg cgc ggc ctc tta acg ctg ctg ctg      51
      Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu
      -20              -15              -10
ccg ccg cca ccc ctg tat acc cgg cac cgc atg ctc ggt cca gag tcc      99
Pro Pro Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser
      -5              1              5
gtc ccg ccc cca aaa cga tcc cgc agc aaa ctc atg gca ccg ccc cga      147
Val Pro Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg
10              15              20              25
atc ggg acg cac aat ggc acc ttc cac tgc gac gag gca ctg gca tgc      195
Ile Gly Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys
      30              35              40
gca ctg ctt cgc ctc ctg ccg gag tac cgg gat gca gag att gtg cgg      243
Ala Leu Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg
      45              50              55
acc cgg gat ccc gaa aaa ctc gct tcc tgt gac atc gtg gtg gac gtg      291
Thr Arg Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val
      60              65              70
ggg ggc gag tac gac cct cgg aga cac cga tat gac cat cac cag agg      339
Gly Gly Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg
      75              80              85
tct ttc aca gag acc atg agc tcc ctg tcc cct ggg agg ccg tgg cag      387
Ser Phe Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln
90              95              100              105
acc aag ctg agc agt gcg gga ctc atc tat ctg cac ttc ggg cac aag      435
Thr Lys Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys

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	110		115		120	
ctg ctg gcc cag ttg ctg ggc act agt gaa gag gac agc atg gtg ggc						483
Leu Leu Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly						
	125		130		135	
acc ctc tat gac aag atg tat gag aac ttt gtg gag gag gtg gat gct						531
Thr Leu Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala						
	140		145		150	
gtg gac aat ggg atc tcc cag tgg gca gag ggg gag cct cga tat gca						579
Val Asp Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala						
	155		160		165	
ctg acc act acc ctg agt gca cga gtt gct cga ctt aat cct acc tgg						627
Leu Thr Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp						
	170		175		180	185
aac cac ccc gac caa gac act gag gca ggg ttc aag cgt gca atg gat						675
Asn His Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp						
	190		195		200	
ctg gtt caa gag gag ttt ctg cag aga tta gat ttc tac caa cac agc						723
Leu Val Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser						
	205		210		215	
tgg ctg cca gcc cgg gcc ttg gtg gaa gag gcc ctt gcc cag cga ttc						771
Trp Leu Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe						
	220		225		230	
cag gtg gac cca agt gga gag att gtg gaa ctg gcg aaa ggt gca tgt						819
Gln Val Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys						
	235		240		245	
ccc tgg aag gag cat ctc tac cac ctg gaa tct ggg ctg tcc cct cca						867
Pro Trp Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro						
	250		255		260	265
gtg gcc atc ttc ttt gtt atc tac act gac cag gct gga cag tgg cga						915
Val Ala Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg						
	270		275		280	
ata cag tgt gtg ccc aag gag ccc cac tca ttc caa agc cgg ctg ccc						963
Ile Gln Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro						
	285		290		295	
ctg cca gag cca tgg cgg ggt ctt cgg gac gag gcc ctg gac cag gtc						1011
Leu Pro Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val						
	300		305		310	
agt ggg atc cct ggc tgc atc ttc gtc cat gca agc ggc ttc att ggc						1059
Ser Gly Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly						
	315		320		325	
ggc cac cgc acc cga gag ggt gcc ttg agc atg gcc cgt gcc acc ttg						1107
Gly His Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu						
	330		335		340	345
gcc cag cgc tca tac ctc cca caa atc tcc tagtctaata aaaccttcca						1157
Ala Gln Arg Ser Tyr Leu Pro Gln Ile Ser						
	350		355			
tctcaaaaaa aaaaaa						1173

<210> 118
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 72..704

<220>
 <221> sig_peptide
 <222> 72..161
 <223> Von Heijne matrix
 score 13.2
 seq LLLSTLVIPSAA/AP

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 <221> polyA_signal
 <222> 772..777

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 aggggcgggg t atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat 110
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His
 -30 -25 -20
 ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct 158
 Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala
 -15 -10 -5
 gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc 206
 Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu
 1 5 10 15
 aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa 254
 Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys
 20 25 30
 ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac 302
 Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp
 35 40 45
 ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag cac 350
 Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His
 50 55 60
 cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag gta 398
 Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val
 65 70 75
 ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg 446
 Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
 80 85 90 95
 gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att 494
 Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
 100 105 110
 aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac 542
 Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
 115 120 125
 tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc 590
 Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
 130 135 140
 cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc 638
 Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser
 145 150 155
 tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc 686
 Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
 160 165 170 175
 agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 734
 Arg Pro Ser Arg Gln Leu
 180
 tagcccccat cagaccctgc cccaagcacc atatggaaat aaagttcttt c 785

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<210> 120
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<212> DNA
<213> Homo sapiens
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<220>
 <221> CDS
 <222> 25..393

<220>
 <221> sig_peptide
 <222> 25..150
 <223> Von Heijne matrix
 score 4.6
 seq LDPAVSLSAPAFA/SA

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 <221> polyA_signal
 <222> 734..739

<220>
 <221> polyA_site
 <222> 757..770

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 Met Lys Gly Gly Ala Phe Ser Asn Leu
 -40 -35
 aat gat tcc cag ctc tca gcc tcg ttt ctg caa ccc agc ctg caa gca 99
 Asn Asp Ser Gln Leu Ser Ala Ser Phe Leu Gln Pro Ser Leu Gln Ala
 -30 -25 -20
 aac tgt cct gct ttg gac cct gct gtg tca ctc tcc gca cca gcc ttt 147
 Asn Cys Pro Ala Leu Asp Pro Ala Val Ser Leu Ser Ala Pro Ala Phe
 -15 -10 -5
 gcc tct gct ctt cgc tct atg aag tcc tcc cag gct gca cgg aag gac 195
 Ala Ser Ala Leu Arg Ser Met Lys Ser Ser Gln Ala Ala Arg Lys Asp
 1 5 10 15
 gac ttt ctc agg tct ctt agt gat gga gac tca ggg aca tca gaa cac 243
 Asp Phe Leu Arg Ser Leu Ser Asp Gly Asp Ser Gly Thr Ser Glu His
 20 25 30
 atc tca gcg gtg gtg act agc cct cgg att tcc tgc cat ggt gct gcc 291
 Ile Ser Ala Val Val Thr Ser Pro Arg Ile Ser Cys His Gly Ala Ala
 35 40 45
 att ccc acc gcc cgt gcc ctc tgc cta ggc tgt tcc tgc tgc acc gaa 339
 Ile Pro Thr Ala Arg Ala Leu Cys Leu Gly Cys Ser Cys Cys Thr Glu
 50 55 60
 cgc ctc ctc ctg cca ccg ccc tcc ctc ctt tct tta gaa gcc cct gcc 387
 Arg Leu Leu Leu Pro Pro Pro Ser Leu Leu Ser Leu Glu Ala Pro Ala
 65 70 75
 agc acc tgagctctct gctgattgct gttcctccca gtctgtggaa gctttgccca 443
 Ser Thr
 80
 tatgctttcc ttaaaagggt tctgggcagg gcaggcgccc ccattttctca gggatcccct 503
 ccaggacaac gccttttccct tgtgtcttca gctctcctta ccagatatct atatatttgt 563
 atatattcag tttcaccaac aatgcatcaa gtactttttt ttttaagtaa agaaccgcag 623
 tcatcgaact ggagcccat tgattccctc cccctcgcc ccccaaactt ggcacctgcc 683
 caaggtatcc tcagaacat ttgggggtgtc ctttggcatt ggataataga aataaaat 743
 tacctctttc tacaataaaa aaaaaaac 770

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<220>

<221> CDS

<222> 58..1095

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<222> 58..114

<223> Von Heijne matrix

score 5.4

seq LSHLLPSLRQVIQ/EP

<220>

<221> polyA_site

<222> 1202..1213

<400> 121

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atg gcc atg gcc cag aaa ctc agc cac ctc ctg ccg agt ctg cgg cag	105
Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln	
-15 -10 -5	
gtc atc cag gag cct cag cta tct ctg cag cca gag cct gtc ttc acg	153
Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr	
1 5 10	
gtg gat cga gct gag gtg ccg ccg ctc ttc tgg aag ccg tac atc tat	201
Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr	
15 20 25	
gcg ggc tac cgg ccg ctg cat cag acc tgg cgc ttc tat ttc cgc acg	249
Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr	
30 35 40 45	
ctg ttc cag cag cac aac gag gcc gtg aat gtc tgg acc cac ctg ctg	297
Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu	
50 55 60	
gcg gcc ctg gta ctg ctg ctg ccg ctg gcc ctc ttt gtg gag acc gtg	345
Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val	
65 70 75	
gac ttc tgg gga gac cca cac gcc ctg ccc ctc ttc atc att gtc ctt	393
Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu	
80 85 90	
gcc tct ttc acc tac ctc tcc ctc agt gcc ttg gct cac ctc ctg cag	441
Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln	
95 100 105	
gcc aag tct gag ttc tgg cat tac agc ttc ttc ttc ctg gac tat gtg	489
Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val	
110 115 120 125	
ggg gtg gcc gtg tac cag ttt ggc agt gcc ttg gca cac ttc tac tat	537
Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr	
130 135 140	
gct atc gag ccc gcc tgg cat gcc cag gtg cag gct gtt ttt ctg ccc	585
Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro	
145 150 155	
atg gct gcc ttt ctc gcc tgg ctt tcc tgc att ggc tcc tgc tat aac	633
Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn	
160 165 170	
aag tac atc cag aaa cca ggc ctg ctg ggc cgc aca tgc cag gag gtg	681
Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val	

175	180	185	
ccc tcc gtc ctg gcc tac gca ctg gac att agt cct gtg gtg cat cgt			729
Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg			
190	195	200	205
atc ttc gtg tcc tcc gac ccc acc acg gat gat cca gct ctt ctc tac			777
Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr			
210	215	220	
cac aag tgc cag gtg gtc ttc ttt ctg ctg gct gct gcc ttc ttc tct			825
His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser			
225	230	235	
acc ttc atg ccc gag cgc tgg ttc cct ggc agc tgc cat gtc ttc ggg			873
Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly			
240	245	250	
cag ggc cac caa ctt ttc cat atc ttc ttg gtg ctg tgc acg ctg gct			921
Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala			
255	260	265	
cag ctg gag gct gtg gca ctg gac tat gag gcc cga cgg ccc atc tat			969
Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr			
270	275	280	285
gag cct ctg cac acg cac tgg cct cac aac ttt tct ggc ctc ttc ctg			1017
Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu			
290	295	300	
ctc acg gtg ggc agc agc atc ctc act gca ttc ctc ctg agc cag ctg			1065
Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu			
305	310	315	
gta cag cgc aaa ctt gat cag aag acc aag tgaaggggga tggcatctgg			1115
Val Gln Arg Lys Leu Asp Gln Lys Thr Lys			
320	325		
tagggagggga ggtatagttg ggggacaggg gtctgggttt ggctccaagt gggaacaagg			1175
cctggtaaag ttgtttgtgt ctggccaaaa aaaaaaaaa			1213

<210> 122
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..660

<220>
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 <222> 31..90
 <223> Von Heijne matrix
 score 5.4
 seq AFVIACVLSLIST/IY

<220>
 <221> polyA_signal
 <222> 1288..1293

<220>
 <221> polyA_site
 <222> 1307..1318

<400> 122
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	Met	Asp	Asn	Arg	Phe	Ala	Thr	Ala	
	-20					-15			
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca									102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala									
	-10			-5		1			
gct tcc att ggc aca gac ttc tgg tat gag tat cga agt cca gtt caa									150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln									
5		10			15		20		
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt									198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser									
	25		30		35				
gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat									246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn									
	40		45		50				
ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg									294
Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met									
	55		60		65				
cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca									342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr									
	70		75		80				
aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt									390
Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val									
	85		90		95		100		
gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt									438
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu									
	105		110		115				
tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc									486
Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys									
	120		125		130				
ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat									534
Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr									
	135		140		145				
ccc acc att gcc acg ggc att ctc cat ctc ctt gca gtg aca aag gag									582
Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Val Thr Lys Glu									
	150		155		160				
agc atg ctt cca gct gga gct gag tcc aag cac aca gcc act cct gca									630
Ser Met Leu Pro Ala Gly Ala Glu Ser Lys His Thr Ala Thr Pro Ala									
	165		170		175		180		
cac gca tgc gtg caa aca ggg aag ccc aag taggagaaga ggaaagaggt									680
His Ala Cys Val Gln Thr Gly Lys Pro Lys									
	185		190						
tgtaggaggatt tgggaagaac cttgattatt ccctggagga aaagacaaat ctacttcctt									740
gaaatcaccc tcgaatctac ttccaccctc agaacttaaa atgaactgca tccttttttt									800
catcttcttt tcttctccag tgaatatgat ctccaaaccc ttattttttt tttgaactgt									860
aaaattttcca ctcatggacg atgcaaccaa cagatgcaat ctctgagaag atgaaaattg									920
ggacctctta ttataaaatt gacctagctg gactcaggaa accaggggaag aagtcaatgc									980
aggcatttaa aatgtaaagt tttttctggt taaatctatt tatttttctt gtaggttgag									1040
tattttcttc cagtttttct gctctggtgt ataacaaaca ggtcaaaatt tcccatcttt									1100
cctcctgata gtagttgaat cctaccttgc atacttaatg catagtgaag tggcatctag									1160
cagaaataca ccccccaaa acacaccacc atttcattag gtgccccaaa aattctgtat									1220
ttagcttatt tatttattgt tatttttgct ttttcttaac ccactatata ttgactgcaa									1280
acgaattaat aaattatccc ttctggaaaa aaaaaaaa									1318

<210> 123

<211> 853

<212> DNA

<213> Homo sapiens

<220>
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 <222> 31..582

<220>
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 <222> 31..90
 <223> Von Heijne matrix
 score 5.4
 seq AFVIACVLSLIST/IY

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 <222> 816..821

<220>
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 <222> 840..853

<400> 123
 ggaggatggg cgagcagtct gaatgccaga atg gat aac cgt ttt gct aca gca 54
 Met Asp Asn Arg Phe Ala Thr Ala
 -20 -15
 ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca 102
 Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
 -10 -5 1
 gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa 150
 Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
 5 10 15 20
 gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt 198
 Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
 25 30 35
 gat gaa gca gat gaa aag act tat aat gat gca cct ttt cga tac aat 246
 Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Pro Phe Arg Tyr Asn
 40 45 50
 ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg 294
 Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met
 55 60 65
 cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca 342
 His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr
 70 75 80
 aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt 390
 Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val
 85 90 95 100
 gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt 438
 Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu
 105 110 115
 tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc 486
 Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys
 120 125 130
 ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat 534
 Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr
 135 140 145
 ccc acc att gcc acg ggc att ctc cat ctc ctt gca gat acc atg ctg 582
 Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Asp Thr Met Leu
 150 155 160

tgaagtccag gccacatgga ggtgtcctgt gtagatgctc cagctgaaat cccaagctaa	642
gctcccaact gacagccaac atcattttcca gccatgtgtg ggagccatcc tggatgtcca	702
gccttaacaa gccttcagag gacttcagcc acagctatta tcttactaca tccttgtgag	762
actctaataa agaaccaact agctgagccc aatcaaccta tggaactgat agaaataaaa	822
tgaattgttg ttttgcgaaa aaaaaaaaaa a	853

<210> 124
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 <212> DNA
 <213> Homo sapiens

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 <222> 15..695

<220>
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 <222> 15..80
 <223> Von Heijne matrix
 score 8.5
 seq AALLLGLMMVVTG/DE

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 <222> 795..800

<220>
 <221> polyA_site
 <222> 814..826

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Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu	
-20 -15	
tta ctg ggt ctc atg atg gtg gtc act gga gac gag gat gag aac agc	98
Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser	
-10 -5 1 5	
ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag	146
Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln	
10 15 20	
ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt	194
Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val	
25 30 35	
gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag	242
Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu	
40 45 50	
ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg	290
Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu	
55 60 65 70	
gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga	338
Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg	
75 80 85	
ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag	386
Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys	
90 95 100	
aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc	434
Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser	

105	110	115	
cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt			482
Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu			
120	125	130	
cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga			530
Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg			
135	140	145	150
ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa			578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu			
155	160	165	
cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca			626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro			
170	175	180	
acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac			674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn			
185	190	195	
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt			725
Gln Ala Glu Ile Ala Ala Cys			
200	205		
ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccctt			785
tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a			826

<210> 125

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 74..295

<220>

<221> sig_peptide

<222> 74..196

<223> Von Heijne matrix

score 5.4

seq RLLYIGFLGYCSG/LI

<220>

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<222> 545..550

<220>

<221> polyA_site

<222> 561..571

<400> 125

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aaacggcgctc acc atg atc gca cgg cgg aac cca gta ccc tta cgg ttt 109

Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe

-40

-35

-30

ctg ccg gat gag gcc cgg agc ctg ccc ccg ccc aag ctg acc gac ccg 157

Leu Pro Asp Glu Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro

-25

-20

-15

cgg ctc ctc tac atc ggc ttc ttg ggc tac tgc tcc ggc ctg att gat 205

Arg Leu Leu Tyr Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp

-10

-5

1

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aac ctg atc cgg cgg agg ccg atc gcg acg gct ggt ttg cat cgc cag      253
Asn Leu Ile Arg Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln
   5             10             15
ctt cta tat att acg gcc ttt ttt ttg ctg gat att atc ttg      295
Leu Leu Tyr Ile Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
  20             25             30
taaaacgtga agactacctg tatgctgtga gggaccgtga aatgtttgga tatatgaaat      355
tacatccaga ggattttcct gaagaagata agaaaacata tggtgaaatt tttgaaaaat      415
tccatccaat acgttgaagt cttcaaaatg cttgctccag tttcactgat acctgctgtt      475
cctgaatttg atggaacatg tttcttatga cagttgaagc ttatgctaatt ctgtatgttg      535
acaccttgta attaaaatac gtaccaaaaa aaaaaa      571

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<210> 126
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 <212> DNA
 <213> Homo sapiens

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 <222> 440..658

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 <221> polyA_signal
 <222> 601..606

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<400> 126
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ttcacagggtg ttggtgcctg ccgtgaacgc attctgacct gggccgtatc tgtctcccaa      120
gactttgtgc ctatggttgg ggacagagtg aggtcgttgc cttgacgacg acagcatgcg      180
gcccggtggtc ctccctaagtg tgagcttgcg gcggaccgag gcccacctgc ctccctgcct      240
gcttcgcca ggactcgtga ctgcgtccgc agaagaaatc acaacagcgc tggaattgct      300
agtttgctag gcagcatctt ttggacctgc gaaccatatg catttcacct caaatctgtt      360
tccaagttga aaacctttgg gtctttctat gcgaacggat tgaagaaacg caaaaagttt      420
ctacggactt taaattaaa atg gaa aaa tat gaa aac ctg ggt ttg gtt gga      472
                Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly
                  1             5             10
gaa ggg agt tat gga atg gtg atg aag tgt agg aat aaa gat act gga      520
Glu Gly Ser Tyr Gly Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly
                15             20             25
aga att gtg gcc ata aag aag ttc tta gaa agt gac gat gac aaa atg      568
Arg Ile Val Ala Ile Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met
                30             35             40
gtt aaa aag att gca atg cga gaa gtc aag tta cta aag caa ctt agg      616
Val Lys Lys Ile Ala Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg
                45             50             55
cat gaa aac ttg gtg aat ctc ttg gaa gtg tgt aaa aaa aaa a      659
His Glu Asn Leu Val Asn Leu Leu Glu Val Cys Lys Lys Lys
  60             65             70

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<210> 127
 <211> 301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..283

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<220>
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<222> 38..85
<223> Von Heijne matrix
      score 4.1
      seq LLPATSLAGPVLS/TL

<220>
<221> polyA_signal
<222> 257..262

<400> 127
cacctgaatc ccaggaaccc tcaatgaggt cttcaag atg aag aga ctg ctg cca      55
                                   Met Lys Arg Leu Leu Pro
                                   -15
gct acc agc ctg gct ggc cct gtc ctg tcc acc ctc att gcc cca act      103
Ala Thr Ser Leu Ala Gly Pro Val Leu Ser Thr Leu Ile Ala Pro Thr
-10                               -5                               1                               5
ccc atg ttg ttt tgt gaa gat aaa agc tgg gat ctt ttt ctt ttt ttt      151
Pro Met Leu Phe Cys Glu Asp Lys Ser Trp Asp Leu Phe Leu Phe Phe
                               10                               15                               20
aag tct cac aag aca tgg ggc atc tcc aca aat tta agt tcc tgt cca      199
Lys Ser His Lys Thr Trp Gly Ile Ser Thr Asn Leu Ser Ser Cys Pro
                               25                               30                               35
ttt gga aat ttg ttt cta tgt gta cag ttt gtc aga gaa aaa caa agt      247
Phe Gly Asn Leu Phe Leu Cys Val Gln Phe Val Arg Glu Lys Gln Ser
                               40                               45                               50
ttt tgt atg aat aca gaa tgt gat tta cgc aag aat tgacaaaaaa      293
Phe Cys Met Asn Thr Glu Cys Asp Leu Arg Lys Asn
55                               60                               65
aaaaaaaaa                                                                301

<210> 128
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 121..477

<220>
<221> sig_peptide
<222> 121..288
<223> Von Heijne matrix
      score 3.5
      seq SSCADSFVSSSSS/QP

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cctcggagca ggcggagtaa agggacttga gcgagccagt tgccggatta ttctatttcc      60
cctccctctc tcccgccccg tatctctttt cacccttctc ccaccctcgc tcgcgtagcc      120
atg gcg gag ccg tcg gcg gcc act cag tcc cat tcc atc tcc tcg tcg      168
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55                               -50                               -45
tcc ttc gga gcc gag ccg tcc gcg ccc ggc ggc ggc ggc ggc agc cca gga      216
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly

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-40	-35	-30	-25	
gcc tgc ccc gcc ctg ggg acg aag agc tgc agc tcc tcc tgt gcg gat	264			
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp				
-20	-15	-10		
tcc ttt gtt tct tcc tct tcc tct cag cct gta tct cta ttt tcg acc	312			
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr				
-5	1	5		
tca caa gag gga ttg agc tct ctt tgc tct gat gag cca tct tca gaa	360			
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu				
10	15	20		
att atg act tct tcc ttt ctt tca tct tct gaa ata cat aac act ggc	408			
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly				
25	30	35	40	
ctt aca ata cta cat gga gaa aaa agc cat gtg tta ggg agc cag cct	456			
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro				
45	50	55		
att tta gcc aaa aaa aaa aaa	477			
Ile Leu Ala Lys Lys Lys Lys				
60				

<210> 129
 <211> 323
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 2..163

<220>
 <221> polyA_signal
 <222> 292..297

<220>
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 <222> 310..323

<400> 129			
a gct ttc gtg tgg gag cca gct atg gtg cgg atc aat gcg ctg aca gca	49		
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala			
1	5	10	15
gcc tct gag gct gcg tgc ctg atc gtg tct gta gat gaa acc atc aag	97		
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys			
20	25	30	
aac ccc cgc tcg act gtg gat gct ccc aca gca gca ggc cgg ggc cgt	145		
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg			
35	40	45	
ggt cgt ggc cgc ccc cac tgagaggcac cccacccatc acatggctgg	193		
Gly Arg Gly Arg Pro His			
50			
ctggctgctg ggtgcactta ccctccttgg cttgggttact tcattttaca aggaaggggt	253		
agtaattggc ccactctctt cttactggag gctattttaa taaaatgtaa gacttcaaaa	313		
aaaaaaaaaa	323		

<210> 130
 <211> 1392
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..675

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<221> sig_peptide

<222> 46..87

<223> Von Heijne matrix

score 5.3

seq LTLGLSFIAGL/IV

<220>

<221> polyA_signal

<222> 1364..1369

<220>

<221> polyA_site

<222> 1383..1392

<400> 130

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                                     Met Leu Thr Leu
tta ggc ctt tca ttc atc ttg gca gga ctt att gtt ggt gga gcc tgc      105
Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys
-10          -5          1          5
att tac aag tac ttc atg ccc aag agc acc att tac cgt gga gag atg      153
Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met
          10          15          20
tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag      201
Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
          25          30          35
cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac      249
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp
          40          45          50
aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac      297
Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp
          55          60          65          70
cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg      345
Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu
          75          80          85
gac ttg ttg ctg ggg atc tgc tat ctg atg ccc ctc aat act tct att      393
Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu Asn Thr Ser Ile
          90          95          100
gtt atg cct cca aaa aat ctg gta gag ctc ttt ggc aaa ctg gcg agt      441
Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly Lys Leu Ala Ser
          105          110          115
ggc aga tat ctg cct caa act tat gtg gtt cga gaa gac cta gtt gct      489
Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu Asp Leu Val Ala
          120          125          130
gtg gag gaa att cgt gat gtt agt aac ctt ggc atc ttt att tac caa      537
Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile Phe Ile Tyr Gln
          135          140          145          150
ctt tgc aat aac aga aag tcc ttc cgc ctt cgt cgc aga gac ctc ttg      585
Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg Arg Asp Leu Leu
          155          160          165
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ctg ggt ttc aac aaa cgt gcc att gat aaa tgc tgg aag att aga cac	633
Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp Lys Ile Arg His	
170 175 180	
ttc ccc aac gaa ttt att gtt gag acc aag atc tgt caa gag	675
Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys Gln Glu	
185 190 195	
taagaggcaa cagatagagt gtccttggtg ataagaagtc agagatttac aatatgactt	735
taacattaag gtttatggga tactcaagat atttactcat gcattttactc tattgottat	795
gcttttaaaaa aaggaaaaaa aaaaaactac taaccactgc aagctcttgt caaatttttag	855
tttaattggc attgcttggt ttttgaaact gaaattacat gagtttcatt ttttctttgc	915
atztataggg tttagatttc tgaaagcagc atgaatatat cacctaacat cctgacaata	975
aattccatcc gttgtttttt ttgtttgttt gttttttctt ttcctttaag taagctcttt	1035
attcatctta tgggtggagca attttaaaat ttgaaatatt ttaaattggt tttgaacttt	1095
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ctttcttgaa tttagaaatt acatctttgc agttctgtta ggtgctctgt aattaacctg	1215
acttatatgt gaacaatttt catgagacag tcattttttaa ctaatgcagt gattctttct	1275
cactactatc tgtattgtgg aatgcacaaa attgtgtagg tgctgaatgc tgtaaggagt	1335
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<222> 974..979	
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<222> 987..999	
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g atg gga tgt gtt ttc cag agc aca gaa gac aaa tgt ata ttc aag ata	109
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile	
1 5 10 15	
gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta	157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu	
20 25 30	
tac tat tac tcc aat ctg agt gtg cct att ggg cgc ttc cag aac cgc	205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg	
35 40 45	
gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctg ctg ctg	253
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu	
50 55 60	
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc	301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg	
65 70 75 80	
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg	349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val	
85 90 95	
ctt cca gag gag ccc aaa ggt acg caa atg ctt act taaagagggg	395

Leu	Pro	Glu	Glu	Pro	Lys	Gly	Thr	Gln	Met	Leu	Thr	
		100				105						
ccaaggggca	agagctttca	tgtgcaagag	gcaaggaac	tgattatctt	gagtaaagtc							455
cagccttttg	gctaagtact	taccacagag	tgaatcttca	aaaaatgac	ataattattt							515
cagtcaataa	aaatagagtt	atthttattaa	ataaaatatt	gataattatt	gtattattac							575
tttaaacaca	cttccccctc	acaaaagccc	tgtgaaggat	gttttggtca	catatatgtc							635
caaatatgtt	ttggacacat	atthttattaa	tggataaat	agtacttgaa	ccctggcacc							695
tctgacaaca	aagtccatgt	tctttttact	atgcctaat	acctttcatc	agttatccac							755
attgatgcta	catctgtatt	ttataggtac	cctatggttag	gtgttctggg	ggatagaaaa							815
gaaataagca	ggccaggctc	agtggctcat	gcctgtaatc	ctagcatttt	gggaggctga							875
ggcagcagaa	ctgcctgagc	cccagggttc	aagactgcag	tgagctatga	tggcaccact							935
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aaaa												999

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 <212> DNA
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<220>
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 <222> 422..550

<220>
 <221> sig_peptide
 <222> 422..475
 <223> Von Heijne matrix
 score 4.5
 seq LRWLMPVIPALWG/AE

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 <221> polyA_site
 <222> 714..725

<400> 132												
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tagccagata	ggtgagtaa	tatatthtga	gtaacctatt	tgctattcct	tgctgcaact							120
gtgtttaatg	ttccttcag	aatcagagag	agtattgcca	tccaagaaat	cgthttttaga							180
tatgacattt	gagctatcat	cttgagacca	atacctaaaa	caatttcagt	ttaagaaatg							240
tctaggtatg	gtgaaaacac	agthttaaaac	cagcaaaaca	gaatttattg	ccctcagcga							300
ataccacaaa	tgtacatata	ccttgatattt	ctgaaagcaa	agcaagcatg	ccaagtagtt							360
tttatthtacc	tgtacctata	atacagcaag	gtgaaacagg	atatatthttt	gaagthttaaa							420
a atg tct tca ggc cgg ctg cgg tgg ctc atg cct gta atc cca gca ctt												469
Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu												
	-15		-10		-5							
tgg gga gcc gag aag ggt gaa tca cct gag gtc agc agt ttt gag acc												517
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr												
	1		5		10							
agg ctg gcc aac atg gcg aaa ccc tgt ctc tac tgaaaataca aaaattagct												570
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr												
	15		20		25							
gggtgtggtg gcgggcgcct gtagtcccag ctacttggga gactgaggca ggagaattgc												630
ttgaacacgg aaggcggaag ttgcagtaag ctgagatcgt gccaccgcac accagcttgg												690
gcaacagagt gagactccct ctcaaaaaaa aaaaa												725

<210> 133
 <211> 400

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..231

<220>
 <221> polyA_site
 <222> 387..400

<400> 133
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 tgc atg tct gcc cga atc cct ttt tat aag gac acc agt cag att aga 168
 Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg
 1 5 10 15
 tta ggg tct acc ata ata cct cat ttt aac tta atc acc ttt gta aag 216
 Leu Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys
 20 25 30
 acc ttt ttc caa ata tagtcaactct ctgaggtact gatgggttagg atctcaacat 271
 Thr Phe Phe Gln Ile
 35
 accttttttg ggaggacaca attgaaccca taacaggggtg tttgcaagga agagttaaaa 331
 tttgaaagaa aggtgggtatt tgcttagata gatagggcac agctttctag gtgacaaaaa 391
 aaaaaaaaaa 400

<210> 134
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 131..1051

<220>
 <221> sig_peptide
 <222> 131..169
 <223> Von Heijne matrix
 score 4.2
 seq MLAVSLTVPLLGA/MM

<220>
 <221> polyA_signal
 <222> 1019..1024

<400> 134
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 gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc 169
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
 -10 -5
 atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa 217
 Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
 1 5 10 15
 gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga 265

Glu	Pro	Pro	Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	
			20					25					30			
cag	gca	gaa	agg	ctg	ttt	gaa	aat	caa	ctt	gtt	gga	ccg	gag	tcc	ata	313
Gln	Ala	Glu	Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	
		35					40					45				
gca	cat	att	ggg	gat	gtg	atg	ttt	act	ggg	aca	gca	gat	ggc	cgg	gtc	361
Ala	His	Ile	Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	
	50					55					60					
gta	aaa	ctt	gaa	aat	ggg	gaa	ata	gag	acc	att	gcc	cgg	ttt	ggg	tgc	409
Val	Lys	Leu	Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	
65					70				75						80	
ggc	cct	tgc	aaa	acc	cga	gat	gat	gag	cct	gtg	tgt	ggg	aga	ccc	ctg	457
Gly	Pro	Cys	Lys	Thr	Arg	Asp	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	
			85					90					95			
ggg	atc	cgt	gca	ggg	ccc	aat	ggg	act	ctc	ttt	gtg	gcc	gat	gca	tgc	505
Gly	Ile	Arg	Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Cys	
			100				105					110				
aag	gga	cta	ttt	gaa	gta	aat	ccc	tgg	aaa	cgt	gaa	gtg	aaa	ctg	ctg	553
Lys	Gly	Leu	Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	
		115				120					125					
ctg	tcc	tcc	gag	aca	ccc	att	gag	ggg	aag	aac	atg	tcc	ttt	gtg	aat	601
Leu	Ser	Ser	Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	
	130				135				140							
gat	ctt	aca	gtc	tct	cag	gat	ggg	agg	aag	att	tat	ttc	acc	gat	tct	649
Asp	Leu	Thr	Val	Ser	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	
145					150				155						160	
agc	agc	aaa	tgg	caa	aga	cga	gac	tac	ctg	ctt	ctg	gtg	atg	gag	ggc	697
Ser	Ser	Lys	Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly	
			165				170						175			
aca	gat	gac	ggg	cgc	ctg	ctg	gag	tat	gat	act	gtg	acc	agg	gaa	gta	745
Thr	Asp	Asp	Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	
			180				185					190				
aaa	gtt	tta	ttg	gac	cag	ctg	cgg	ttc	ccg	aat	gga	gtc	cag	ctg	tct	793
Lys	Val	Leu	Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	
		195			200						205					
cct	gca	gaa	gac	ttt	gtc	ctg	gtg	gca	gaa	aca	acc	atg	gcc	agg	ata	841
Pro	Ala	Glu	Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile	
	210				215						220					
cga	aga	gtc	tac	gtt	tct	ggc	ctg	atg	aag	ggc	ggg	gct	gat	ctg	ttt	889
Arg	Arg	Val	Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe	
225					230				235					240		
gtg	gag	aac	atg	cct	gga	ttt	cca	gac	aac	atc	cgg	ccc	agc	agc	tct	937
Val	Glu	Asn	Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser	
			245					250					255			
ggg	ggg	tac	tgg	gtg	ggc	atg	tcg	acc	atc	cgc	cct	aac	cct	ggg	ttt	985
Gly	Gly	Tyr	Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe	
		260				265						270				
tcc	atg	ctg	gat	ttc	tta	tct	gag	aga	ccc	tgg	att	aaa	agg	atg	att	1033
Ser	Met	Leu	Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile	
		275				280					285					
ttt	aag	gca	aaa	aaa	aaa	aa										1053
Phe	Lys	Ala	Lys	Lys	Lys											
		290														

<210> 135
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<213> Homo sapiens

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<221> CDS

<222> 86..403

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<221> sig_peptide

<222> 86..181

<223> Von Heijne matrix

score 8.8

seq VPMLLLIVGGSFG/LR

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<221> polyA_signal

<222> 1097..1102

<220>

<221> polyA_site

<222> 1117..1128

<220>

<221> misc_feature

<222> 427..429

<223> n=a, g, c or t

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tctgagccga tggaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct      112
                               Met Phe Ala Pro Ala Val Met Arg Ala
                               -30                               -25

ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg      160
Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu
                               -20                               -15                               -10

att gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat      208
Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr
                               -5                               1                               5

gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa      256
Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys
10                               15                               20                               25

gag aat aaa ata tct tta gag tgc gaa tat gag aaa atc aaa gac tcc      304
Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser
                               30                               35                               40

aag ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat      352
Lys Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp
                               45                               50                               55

cct gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca      400
Pro Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr
60                               65                               70

act tgactctgct gattcttttt tccnnntttt ttttttttta aataaaaata      453
Thr

ctattaactg gacttcctaa tatatacttc tatcaagtgg aaaggaaatt ccaggcccat      513
ggaaacttgg atatgggtaa tttgatgaca aataatcttc actaaaggtc atgtacaggt      573
ttttatactt cccagctatt ccactctgtg atgaaagtaa caatgttggc cacgtatatt      633
ttacacctcg aaataaaaaa tgtgaatact gctccaaaaa aaaaaaccag taccgtgtag      693
tctctctcgt ggcttggatt tacactgggc aacgtgggtg gaatgtatct ggctcagaac      753
tatgatatac caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaaag      813
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aagaaacccc	ctagtgc	atg	agactgcctc	cagcactgcc	ttcaggatat	accgattcta	873
ctgctcttga	gggcctcggt	tactatctga	acccaaaagct	tttgttttcg	tctccagcct		933
cagcacttct	cttctttgct	agaccctgtg	ttttttgctt	taaagcaagc	aaaatggggc		993
cccaatttga	gaactaccg	acgtttccaa	catactcacc	tcttcccata	atccctttcc		1053
aactgcatgg	gaggttctaa	gactggaatt	atggtgctag	attagtaaac	atgactttta		1113
acgaaaaaaaa	aaaaa						1128

<210> 136
 <211> 254
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..162

<220>
 <221> sig_peptide
 <222> 37..93
 <223> Von Heijne matrix
 score 9.5
 seq LMCLSLCTAFALS/KP

<220>
 <221> polyA_signal
 <222> 224..229

<220>
 <221> polyA_site
 <222> 243..254

<400> 136	
tgtgctgtgg gggctacgag gaaagatcta attatc atg gac ctg cga cag ttt	54
	Met Asp Leu Arg Gln Phe
	-15
ctt atg tgc ctg tcc ctg tgc aca gcc ttt gcc ttg agc aaa ccc aca	102
Leu Met Cys Leu Ser Leu Cys Thr Ala Phe Ala Leu Ser Lys Pro Thr	
	-10 -5 1
gaa aag aag gac cgt gta cat cat gag cct cag ctc agt gac aag gtt	150
Glu Lys Lys Asp Arg Val His His Glu Pro Gln Leu Ser Asp Lys Val	
	5 10 15
cac aat gat att tgatagaacc aattgttgta cataaaacag atctgcgcat	202
His Asn Asp Ile	
20	
atatatatat gtataaaaaa taataaaata atggaagatg aaaaaaaaaa aa	254

<210> 137
 <211> 886
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..381

<220>
 <221> sig_peptide

<222> 31..90
 <223> Von Heijne matrix
 score 5.4
 seq AFVIACVLSLIST/IY

<220>
 <221> polyA_site
 <222> 875..886

<400> 137
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 Met Asp Asn Arg Phe Ala Thr Ala
 -20 -15
 ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca 102
 Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
 -10 -5 1
 gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa 150
 Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
 5 10 15 20
 gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt 198
 Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
 25 30 35
 gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat 246
 Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn
 40 45 50
 ggc aca gtg gga ttg tgg gga cgg tgt atc acc ata ccc aaa aac atg 294
 Gly Thr Val Gly Leu Trp Gly Arg Cys Ile Thr Ile Pro Lys Asn Met
 55 60 65
 cat tgg tat agc cca cca gaa agg aca ggt att tct ctt att tta act 342
 His Trp Tyr Ser Pro Pro Glu Arg Thr Gly Ile Ser Leu Ile Leu Thr
 70 75 80
 tct gtc ttc ttc acc tgg tta ata ata gac aaa acg acg taatgattgc 391
 Ser Val Phe Phe Thr Trp Leu Ile Ile Asp Lys Thr Thr
 85 90 95
 ccaattacat gtaagcaggt ttgttggttc tctctctcct taaagaaata aatcgtgtat 451
 cttctctttc tactgccttc tctccccaac ttctttgcat taccatggta ctcatcaata 511
 ttggttggat gaggaacttt tcttatcttg ggaaagcctt aatggctttt ttttttctta 571
 tttactcact cattaataata cttttcatta ctctaacaca tgttataaag aaatagttgg 631
 aaaagtgcac cgaaagactt ttaaaaaatat ttggttaacta gtaaaaggac taccatcgaa 691
 aatcaactca aaaaattgtc cttttatggg ttagctgtat tataatacat atctatcatt 751
 tgcccctgtg tcttagagga tataatttga ccagctctac atttaatctg tgtaattatg 811
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 gttaaaaaaaa aaaaa 886

<210> 138
 <211> 1244
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 46..579

<220>
 <221> sig_peptide
 <222> 46..156
 <223> Von Heijne matrix

score 3.5
seq LVFNFLILTILT/IW

<220>

<221> misc_feature

<222> 15,23,32..34,102..104,110,114,1019,1029..1030,1093,1209,1236

<223> n=a, g, c or t

<400> 138

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                                   Met Glu Arg Gln
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tca agg gtt atg tca gaa aag gat gag tat cag ttt caa cat can nna      105
Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe Gln His Xaa Xaa
                                   -30               -25               -20
gcg gng gan ctg ctt gtc ttc aat ttt ttg ctc atc ctt acc att ttg      153
Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile Leu Thr Ile Leu
                                   -15               -10               -5
aca atc tgg tta ttt aaa aat cat cga ttc cgc ttc ttg cat gaa act      201
Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe Leu His Glu Thr
                                   1               5               10               15
gga gga gca atg gtg tat ggc ctt ata atg gga cta att tca cga tat      249
Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu Ile Ser Arg Tyr
                                   20               25               30
gct aca gca cca act gat att gaa agt gga act gtc tgt gac tgt gta      297
Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val Cys Asp Cys Val
                                   35               40               45
aaa cta act ttc agt cca cca act ctg ctg gtt aat gtc act gac caa      345
Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn Val Thr Asp Gln
                                   50               55               60
gtt tat gaa tat aaa tac aaa aga gaa ata agt cag cac aac atc aat      393
Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln His Asn Ile Asn
                                   65               70               75
cct cat caa gga aat gct ata ctt gaa aag atg aca ttt gat cca gaa      441
Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr Phe Asp Pro Glu
                                   80               85               90               95
atc ttc ttc aat gtt tta ctg cca cca att ata ttt cat gca gga tat      489
Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe His Ala Gly Tyr
                                   100              105              110
agt cta aag aag aga cac ttt ttt caa aac tta gga tct att tta acg      537
Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly Ser Ile Leu Thr
                                   115              120              125
tat gcc ttc ttg gga act gcc atc tcc tgc atc gtc ata ggg      579
Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val Ile Gly
                                   130              135              140
taagtacat tccgagctca agttgcaggt ggctgtgggg tctgtgatct gtgtgagga      639
tctaacactt ccaggattct tgctggctgg gaaaattgtc ttttttttag tatatcacat      699
atttgatatgt tttttctgac ttaattccac ggcttctgac aaatacaagg cttcaaataca      759
aagcaaacta gaggattgct ggactttctc tgtgagttct ggacttctga cttaggggaat      819
gtggatcact tgccttgagt tatgtgaagc gcattgcatt cttcttttag tttgagtaat      879
gccgatatgg tcaactgcatt cttttttgtc ttgtattgag agaccttacc tgtatttggc      939
aggagtgcaa aagtaactat atgccaagag ttttctttct aaaggaaagt ttacaagaca      999
gcagtctgaa acagatatgn tccaaatatn naacagagtt gcttaataca gggatagctt     1059
ttcagttaat accctgtaga atgcagactc tttntttcat tgtattttct tgattatgct     1119
actgagccct aagtcacacg ttatatactc tggtctgcag ctcatacataa agtaaaatgt     1179
ggtaccaaat ggtgaaggca atccagcctn tgataatccc gtccaataca ttaaagntcc     1239
actgc                                                                1244
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<210> 139
 <211> 471
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 92..469

<220>
 <221> sig_peptide
 <222> 92..172
 <223> Von Heijne matrix
 score 7.9
 seq VVVLALGFLGCGY/AK

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 <221> polyA_signal
 <222> 454..459

<220>
 <221> polyA_site
 <222> 458..471

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 gaagatcttc gggccactgt cgtccagtgc c atg cag ttt gtc aac gtg ggc 112
 Met Gln Phe Val Asn Val Gly
 -25
 tac ttc ctc atc gca gcc ggc gtt gtg gtc ctt gct ctt ggt ttc ctg 160
 Tyr Phe Leu Ile Ala Ala Gly Val Val Val Leu Ala Leu Gly Phe Leu
 -20 -15 -10 -5
 ggc tgc tat ggt gct aag act gag agc atg tgt gcc ctc gtg acg ttc 208
 Gly Cys Tyr Gly Ala Lys Thr Glu Ser Met Cys Ala Leu Val Thr Phe
 1 5 10
 ttc ttc atc ctc ctc ctc atc ttc att gct gag gtt gca gct gct gtg 256
 Phe Phe Ile Leu Leu Leu Ile Phe Ile Ala Glu Val Ala Ala Ala Val
 15 20 25
 gtc gcc ctg gtg tac acc aca atg gct gag cac ttc ctg acg ttg ctg 304
 Val Ala Leu Val Tyr Thr Thr Met Ala Glu His Phe Leu Thr Leu Leu
 30 35 40
 gta gtg cct gcc atc aag aaa gat tat ggt tcc cag gaa gac ttc act 352
 Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp Phe Thr
 45 50 55 60
 caa gtg tgg aac acc acc atg aaa ggg ctc aag tgc cgt ggc ttc acc 400
 Gln Val Trp Asn Thr Thr Met Lys Gly Leu Lys Cys Arg Gly Phe Thr
 65 70 75
 aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg cat aaa cct 448
 Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met His Lys Pro
 80 85 90
 gtt aca atg aaa aaa aaa aa 471
 Val Thr Met Lys Lys Lys Lys
 95

<210> 140
 <211> 849

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..675

<220>
 <221> sig_peptide
 <222> 154..498
 <223> Von Heijne matrix
 score 4.8
 seq PLRLLNLLILIEG/GV

<220>
 <221> polyA_signal
 <222> 819..824

<220>
 <221> polyA_site
 <222> 838..849

<400> 140
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 agaatcaagg aggttctctt caactccctc ttcagtgcct actatgttgc atttctcccc 120
 ctgtgttttg tgaagagtac ccagtactat gac atg cgc tgg tca tgt gag cac 174
 Met Arg Trp Ser Cys Glu His
 -115 -110
 ctc gtt atg gtg tgg atc aat gct ttt gtc atg ctc acc acg caa ctg 222
 Leu Val Met Val Trp Ile Asn Ala Phe Val Met Leu Thr Thr Gln Leu
 -105 -100 -95
 ttg cca tcc aaa tac tgt gat ttg cta cat aaa tca gct gct cac ctg 270
 Leu Pro Ser Lys Tyr Cys Asp Leu Leu His Lys Ser Ala Ala His Leu
 -90 -85 -80
 ggc aag tgg cag aag ttg gaa cat ggg tcc tac agc aat gct cca cag 318
 Gly Lys Trp Gln Lys Leu Glu His Gly Ser Tyr Ser Asn Ala Pro Gln
 -75 -70 -65
 cac att tgg tca gaa aat aca ata tgg cct caa ggg gtg ctg gtg cgg 366
 His Ile Trp Ser Glu Asn Thr Ile Trp Pro Gln Gly Val Leu Val Arg
 -60 -55 -50 -45
 cac agc aga tgt tta tat aga gcc atg ggg cct tac aac gtg gca gtg 414
 His Ser Arg Cys Leu Tyr Arg Ala Met Gly Pro Tyr Asn Val Ala Val
 -40 -35 -30
 cct tca gat gta tct cat gcc cgc ttt tat ttc tta ttt cat cga cca 462
 Pro Ser Asp Val Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro
 -25 -20 -15
 tta agg ctg tta aat ctg ctc atc ctt att gag ggc ggt gtc gtc ttc 510
 Leu Arg Leu Leu Asn Leu Leu Ile Leu Ile Glu Gly Gly Val Val Phe
 -10 -5 1
 tat cag ctc tat tcc ttg ctg cgg tgc gag aag tgg aac cac aca ctt 558
 Tyr Gln Leu Tyr Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu
 5 10 15 20
 tcc atg gct ctc atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt 606
 Ser Met Ala Leu Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu
 25 30 35
 ctc cgg gac aga ata gta tta ggc agg gca tac tcc tac cca ctc aac 654
 Leu Arg Asp Arg Ile Val Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn

40 45 50 705
 agt tat gaa ctc aag gca aac taagctgcct ctcaacaatg agggagaact
 Ser Tyr Glu Leu Lys Ala Asn

55 765
 cagataaaaa tattttcata cgttctatatt ttttcttgatg atttttataa atattttaaga
 tgttttatat tttgtatact attatgtttt gaaagtcggg aagagtaagg gatattaaat 825
 gtatccgtaa acaaaaaaaaa aaaa 849

<210> 141
 <211> 155
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 141
 Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
 -30 -25 -20
 Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
 -15 -10 -5 1
 Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His Ala Val
 5 10 15
 Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
 20 25 30
 Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
 35 40 45
 Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu
 50 55 60 65
 Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
 70 75 80
 Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
 85 90 95
 Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu Phe Leu
 100 105 110
 Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
 115 120

<210> 142
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 142
 Met Ala Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg
 1 5 10 15
 Met Tyr Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe
 20 25 30
 Phe Met Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln
 35 40 45
 Lys Gln Lys Lys Arg Ser Asn
 50 55

<210> 143
 <211> 67
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 143

```
Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
-20          -15          -10          -5
Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg
          1          5          10
Leu Glu Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val
          15          20          25
Gln Glu Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe
          30          35          40
Gly Arg Lys
45
```

<210> 144

<211> 198

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 144

```
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
-20          -15          -10
Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
-5          1          5          10
Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
          15          20          25
Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Trp Leu Thr Lys Ala Arg
          30          35          40
Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
          45          50          55
Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
          60          65          70          75
Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu Gln Ala Glu Ala Thr
          80          85          90
Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
          95          100          105
Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser Ala Trp Leu Gly Pro
          110          115          120
Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His Ala Asp Lys Gln Ser
          125          130          135
His Ile Leu Trp Ala Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu
          140          145          150          155
Met Val Ala Gln Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His
          160          165          170
Thr Ala Ala Leu Pro Ala
          175
```

<210> 145

<211> 135

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<220>
 <221> UNSURE
 <222> 39
 <223> Xaa = any one of the twenty amino acids

<400> 145
 Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
 -25 -20 -15 -10
 Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5
 Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
 10 15 20
 Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Lys Xaa
 25 30 35
 Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn Leu Ser Phe
 40 45 50 55
 Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg Lys Asn Trp
 60 65 70
 Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu Gly Thr Tyr
 75 80 85
 Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln Ser Gln Ser
 90 95 100
 Lys Gln Lys Ser Ile Glu Glu
 105 110

<210> 146
 <211> 255
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -70...-1

<400> 146
 Met Gln Gln Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe
 -70 -65 -60 -55
 Pro Gln Ile Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val
 -50 -45 -40
 Ile Ala Asn Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn
 -35 -30 -25
 Val Val Ser Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu
 -20 -15 -10
 Ala Pro Phe Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val
 -5 1 5 10
 Gly Leu Gly Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val
 15 20 25
 Glu Asn Thr Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr
 30 35 40
 Ala Thr Ser Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp

Glu Ile Leu Arg Met Ala Gly Pro Leu Thr Ala Asp Phe Ile Val Lys
 115 120 125
 Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr Val Gln Phe Ile Phe Tyr
 130 135 140
 Gln Pro Ile Ile His Arg Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser
 145 150 155 160
 Ala Thr Cys Gly Gly Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp
 165 170 175
 Leu Arg Ser Asn
 180

<210> 149
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 149
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 -20 -15 -10
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 -5 1 5
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 10 15 20 25
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 30 35 40
 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 45 50 55
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 60 65 70
 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
 75 80 85
 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Pro Asp Asn
 90 95 100 105
 Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
 110 115 120
 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Val Ser Met
 125 130 135
 Val Phe

<210> 150
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 150
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 -20 -15 -10
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 -5 1 5

Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys	Glu	Cys	Phe
10					15					20					25
Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile	Glu	Tyr	Gln	Val
				30					35					40	
Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His	Leu	Ala	Ser	Pro	Glu
			45					50					55		
Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys	Ser	Asp	Gly	Val	His	Thr
		60					65					70			
Cys	Ile	Arg	Ser	Lys	Asn	Gly	Pro	Gly	Thr	Ala	Val	His	Ala	Tyr	Asn
	75					80					85				
Pro	Ser	Thr	Phe	Arg	Gly	Gln	Val								
90					95										

<210> 151
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 151
 Met Val Glu Met Thr Gly Val
 1 5

<210> 152
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 152

Met	Asp	Gly	Gln	Lys	Lys	Asn	Trp	Lys	Asp	Lys	Val	Val	Asp	Leu	Leu
		-40					-35					-30			
Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe	Gly	Ala	Ser	Leu
	-25					-20					-15				
Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val	Ser	Val	Thr	Ala
-10				-5						1				5	
Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser	Phe	Arg	Ile	Tyr
		10						15					20		
Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu	Gly	His	Pro	Phe
		25					30					35			
Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu	Glu	Leu	Val	Gln
	40					45					50				
Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Cys	Thr	Ile	Lys	Glu
55					60					65				70	
Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe
				75					80					85	
Ala	Val	Leu	Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly
			90					95						100	
Leu	Thr	Leu	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Val	Pro	Val
		105					110						115		
Ile	Tyr	Glu	Arg	His	Gln	Ala	Gln	Ile	Asp	His	Tyr	Leu	Val	Leu	Ala
	120					125					130				
Asn	Lys	Asn	Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile	Pro
135						140				145					150
Gly	Leu	Lys	Arg	Lys	Ala	Glu									

<210> 153
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Pro Phe Arg Met Ser Gly Tyr Ile Pro Phe Gly Thr Pro Ile Val
 1 5 10 15
 Ser Val Thr Phe Lys Gly Phe Pro Phe Leu Lys Asn Tyr Phe Lys Cys
 20 25 30
 Leu Thr Leu Cys Tyr Cys Ser Arg Val Phe Asp
 35 40

<210> 154
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 154
 Met Glu Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro
 -35 -30 -25
 Gly Trp Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe
 -20 -15 -10
 Ser Gly Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala
 -5 1 5 10
 Gln Glu

<210> 155
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 155
 Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
 1 5 10 15
 His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
 20 25 30
 Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
 35 40 45
 Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
 50 55 60
 Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
 65 70 75 80
 Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
 85 90 95
 Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
 100 105 110
 Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
 115 120 125
 Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
 130 135 140

Gln Val Ser Gln Gln Glu Glu Leu Lys
 145 150

<210> 156
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 156
 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Lys Leu Met Met
 1 5 10 15
 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
 20 25 30
 Gly Lys Asp Ile Asp Leu Asn Lys Val Arg Thr Lys Thr Ala Ala Lys
 35 40 45
 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val
 50 55 60
 Pro Pro Glu
 65

<210> 157
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 157
 Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala Arg
 1 5 10 15
 Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val Phe
 20 25 30
 Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys Gly
 35 40 45
 Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln Ala
 50 55 60
 Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp Lys
 65 70 75 80
 Leu Ala Glu Glu His Ser Ser
 85

<210> 158
 <211> 250
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -85..-1

<220>
 <221> UNSURE
 <222> -30
 <223> Xaa = any one of the twenty amino acids

<400> 158
 Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
 -85 -80 -75 -70
 Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His

Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys Ser Arg Asn Leu
 85 90 95
 Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro Ser Ser Leu Lys
 100 105 110
 Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His Ser Tyr Ala Phe
 115 120 125
 Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys Leu Glu Lys Glu
 130 135 140
 Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu Gln Lys Glu Arg
 145 150 155 160
 Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu Val Lys Asn Leu
 165 170 175
 Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu His Met Leu Pro
 180 185 190
 Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys Ile Leu Glu Gln
 195 200 205
 Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu Lys Gln Thr Lys
 210 215 220
 Ser Thr Phe Ile
 225

<210> 161
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 161
 Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
 -20 -15 -10 -5
 Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
 1 5 10
 Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
 15 20 25
 Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
 30 35 40
 Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
 45 50 55 60
 Pro Ala Lys Leu Arg Gln
 65

<210> 162
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Asn
 1 5 10 15
 Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp Val
 20 25 30
 Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
 35 40

<210> 163
 <211> 314
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

<400> 163
 Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
 -55 -50 -45
 Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly
 -40 -35 -30
 Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
 -25 -20 -15
 His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
 -10 -5 1 5
 Ala Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro
 10 15 20
 Cys Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala
 25 30 35
 Ile Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His
 40 45 50
 Asn Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu
 55 60 65 70
 Glu Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu
 75 80 85
 Glu Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr
 90 95 100
 Glu Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg
 105 110 115
 Lys Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp
 120 125 130
 Ala Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys
 135 140 145 150
 Tyr Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg
 155 160 165
 Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His
 170 175 180
 Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro
 185 190 195
 Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys
 200 205 210
 Ile Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met
 215 220 225 230
 Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile
 235 240 245
 Glu Tyr Asp Tyr Thr Arg His Phe Thr Met
 250 255

<210> 164
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -80..-1

<400> 164

Met	Arg	Thr	Arg	Thr	Thr	Gly	Asn	Pro	Arg	Gly	Leu	His	Asp	Thr	Phe	
-80					-75					-70					-65	
Pro	Arg	Arg	Pro	Arg	Leu	Gly	Arg	Cys	Ser	Asp	Met	Asp	Thr	Ala	Arg	
			-60					-55						-50		
Thr	Ser	Cys	Ser	Asp	Leu	Leu	Pro	Trp	Glu	Gly	Val	Thr	Glu	Pro	Ala	
		-45					-40					-35				
Leu	Cys	Gly	Asp	Gln	Leu	Gln	Gly	Thr	Glu	Gly	Trp	Leu	Glu	Ala	Thr	
	-30					-25					-20					
Gln	Leu	Gly	Arg	Gly	Leu	Leu	Ser	Ala	Cys	Ala	Pro	Trp	Gly	Asp	Gly	
-15					-10						-5					
Ser	Thr	Gln	Pro	Val	Pro	Leu	Cys	Ser								
1				5												

<210> 165
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 165

Met	Glu	Ala	Met	Trp	Leu	Leu	Cys	Val	Ala	Leu	Ala	Val	Leu	Ala	Trp	
-15					-10					-5					1	
Gly	Phe	Leu	Trp	Val	Trp	Asp	Ser	Ser	Glu	Arg	Met	Lys	Ser	Arg	Glu	
		5				10						15				
Gln	Gly	Gly	Arg	Leu	Gly	Ala	Glu	Ser	Arg	Thr	Leu	Leu	Val	Ile	Ala	
	20					25					30					
His	Pro	Asp	Asp	Glu	Ala	Met	Phe	Phe	Ala	Pro	Thr	Val	Leu	Gly	Leu	
35					40					45						
Ala	Arg	Leu	Arg	His	Trp	Val	Tyr	Leu	Leu	Cys	Phe	Ser	Ala	Val	Phe	
50				55					60						65	
Arg	Arg	Glu	Leu	Ser	Glu	Tyr	Thr	Glu	Gly	Leu	Thr	Ser	Glu	Pro	Leu	
			70					75					80			
Thr	Ala															

<210> 166
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 166

Met	Leu	Val	Thr	Gln	Gly	Leu	Val	Tyr	Gln	Gly	Tyr	Leu	Ala	Ala	Asn	
-35					-30					-25						
Ser	Arg	Phe	Gly	Ser	Leu	Pro	Lys	Val	Ala	Leu	Ala	Gly	Leu	Leu	Gly	
-20				-15					-10						-5	
Phe	Gly	Leu	Gly	Lys	Val	Ser	Tyr	Ile	Gly	Val	Cys	Gln	Ser	Lys	Phe	
			1				5					10				

His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His
 15 20 25
 Asn Arg His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly
 30 35 40
 Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 45 50 55

<210> 167
 <211> 351
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 167
 Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly
 -15 -10 -5
 Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
 1 5 10 15
 Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
 20 25 30
 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
 35 40 45
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
 50 55 60
 Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro
 65 70 75 80
 Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
 85 90 95
 Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
 100 105 110
 Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
 115 120 125
 Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
 130 135 140
 Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
 145 150 155 160
 Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
 165 170 175
 Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
 180 185 190
 Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
 195 200 205
 Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
 210 215 220
 Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
 225 230 235 240
 Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
 245 250 255
 Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
 260 265 270
 Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
 275 280 285
 Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
 290 295 300

His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Cys
 305 310 315 320
 His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp Arg
 325 330 335

<210> 168
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 168
 Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu
 -45 -40 -35
 Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser
 -30 -25 -20
 Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile
 -15 -10 -5 1
 Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu
 5 10 15
 Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys Tyr Val Ala Gly Ile
 20 25 30
 Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp Asn Val Ser Gly Glu
 35 40 45
 Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser Ala Pro Leu Gln Phe
 50 55 60 65
 Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His Thr Asn Arg Arg Glu
 70 75 80
 Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala
 85 90

<210> 169
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -73..-1

<400> 169
 Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
 -70 -65 -60
 Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
 -55 -50 -45
 Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
 -40 -35 -30
 Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
 -25 -20 -15 -10
 Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
 -5 1 5
 Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
 10 15 20
 Pro Leu Gly Thr Pro

25

<210> 170
 <211> 252
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -68...-1

<400> 170
 Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
 -65 -60 -55
 Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
 -20 -15 -10 -5
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
 1 5 10
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
 15 20 25
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
 45 50 55 60
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
 80 85 90
 Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
 95 100 105
 Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
 110 115 120
 Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
 125 130 135 140
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
 145 150 155
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
 Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
 175 180

<210> 171
 <211> 350
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -68...-1

<400> 171
 Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
 -65 -60 -55

Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
 -20 -15 -10 -5
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
 1 5 10
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
 15 20 25
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
 45 50 55 60
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala
 80 85 90
 Leu Gln Gln His Arg Pro Ser Pro Glu Leu Thr Leu Ser Gln Lys Ile
 95 100 105
 Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu Glu Leu Cys His Ser Val
 110 115 120
 Pro Lys Glu Val Asp Gln Leu Gly Gly Arg Gly Tyr Gly Ser Glu Ser
 125 130 135 140
 Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala Trp Leu Arg Cys Tyr Gly
 145 150 155
 Met Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp
 160 165 170
 Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg
 175 180 185
 Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
 190 195 200
 Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys
 205 210 215 220
 Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
 225 230 235
 Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
 240 245 250
 Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
 255 260 265
 Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
 270 275 280

<210> 172
 <211> 390
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -68...-1

<400> 172
 Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
 -65 -60 -55
 Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
 -50 -45 -40

Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
 -35 -30 -25
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
 -20 -15 -10 -5
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
 1 5 10
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
 15 20 25
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
 45 50 55 60
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
 80 85 90
 Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
 95 100 105
 Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
 110 115 120
 Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
 125 130 135 140
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp
 145 150 155
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
 Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe
 175 180 185
 Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln
 190 195 200
 Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu
 205 210 215 220
 Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln
 225 230 235
 Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
 240 245 250
 Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
 255 260 265
 Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
 270 275 280
 Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
 285 290 295 300
 His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
 305 310 315
 Glu Gly Thr Ser Ala Ser
 320

<210> 173

<211> 190

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -82...-1

<400> 173

Met	Tyr	Val	Trp	Pro	Cys	Ala	Val	Val	Leu	Ala	Gln	Tyr	Leu	Trp	Phe
	-80					-75					-70				
His	Arg	Arg	Ser	Leu	Pro	Gly	Lys	Ala	Ile	Leu	Glu	Ile	Gly	Ala	Gly
	-65					-60					-55				
Val	Ser	Leu	Pro	Gly	Ile	Leu	Thr	Ala	Lys	Cys	Gly	Ala	Glu	Val	Ile
-50					-45					-40					-35
Leu	Ser	Asp	Ser	Ser	Glu	Leu	Pro	His	Cys	Leu	Glu	Val	Cys	Arg	Gln
			-30						-25					-20	
Ser	Cys	Gln	Met	Asn	Asn	Leu	Pro	His	Leu	Gln	Val	Val	Gly	Leu	Thr
		-15						-10					-5		
Trp	Gly	His	Ile	Ser	Trp	Asp	Leu	Leu	Ala	Leu	Pro	Pro	Gln	Asp	Ile
	1				5					10					
Ile	Leu	Ala	Ser	Asp	Val	Phe	Phe	Glu	Pro	Glu	Asp	Phe	Glu	Asp	Ile
15					20					25					30
Leu	Ala	Thr	Ile	Tyr	Phe	Leu	Met	His	Lys	Asn	Pro	Lys	Val	Gln	Leu
			35						40					45	
Trp	Ser	Thr	Tyr	Gln	Val	Arg	Ser	Ala	Asp	Trp	Ser	Leu	Glu	Ala	Leu
		50						55					60		
Leu	Tyr	Lys	Trp	Asp	Met	Lys	Cys	Val	His	Ile	Pro	Leu	Glu	Ser	Phe
	65					70					75				
Asp	Ala	Asp	Lys	Glu	Asp	Ile	Ala	Glu	Ser	Thr	Leu	Pro	Gly	Arg	His
80					85					90					
Thr	Val	Glu	Met	Leu	Val	Ile	Ser	Phe	Ala	Lys	Asp	Ser	Leu		
95				100						105					

<210> 174

<211> 285

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -232..-1

<400> 174

Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Asp	Lys	Arg	Ile	Phe	Lys	Ile
	-230						-225				-220				
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu
-215						-210					-205				
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg
-200				-195						-190					-185
Val	His	Leu	Met	Gly	Asp	Asn	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu
			-180						-175					-170	
Gln	Asp	Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg
	-165							-160					-155		
Leu	Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val
	-150						-145				-140				
Leu	Pro	Glu	Glu	Pro	Lys	Glu	Leu	Met	Val	His	Val	Gly	Gly	Leu	Ile
-135						-130					-125				
Gln	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Val	Lys	His	Val	Thr	Lys
-120				-115						-110					-105
Val	Glu	Trp	Ile	Phe	Ser	Gly	Arg	Arg	Ala	Lys	Glu	Glu	Ile	Val	Phe
			-100						-95					-90	
Arg	Tyr	Tyr	His	Lys	Leu	Arg	Met	Ser	Ala	Glu	Tyr	Ser	Gln	Ser	Trp
		-85					-80					-75			
Gly	His	Phe	Gln	Asn	Arg	Val	Asn	Leu	Val	Gly	Asp	Ile	Phe	Arg	Asn
	-70					-65						-60			

Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
 -55 -50 -45
 Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
 -40 -35 -30 -25
 Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
 -20 -15 -10
 Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
 -5 1 5
 Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
 10 15 20
 Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
 25 30 35 40
 Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys Lys
 45 50

<210> 175
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 175
 Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
 100 105 110
 Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
 115 120 125
 Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
 130 135 140
 His His Cys Val Arg Glu Gly Ser Gly
 145 150

<210> 176
 <211> 49
 <212> PRT
 <213> Homo sapiens

<221> UNSURE
 <222> 3
 <223> Xaa = any one of the twenty amino acids

<400> 176
 Met Leu Xaa Gly Asp His Arg Ala Leu Leu Lys Ile Trp Leu Leu
 1 5 10 15
 Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
 20 25 30
 Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe

<221> SIGNAL
 <222> -23...-1

<400> 179

Met	Met	Leu	Pro	Gln	Trp	Leu	Leu	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Phe
		-20						-15					-10		
Leu	Phe	Leu	Leu	Thr	Arg	Gly	Ser	Leu	Ser	Pro	Thr	Lys	Tyr	Asn	Leu
	-5					1				5					
Leu	Glu	Leu	Lys	Glu	Ser	Cys	Ile	Arg	Asn	Gln	Asp	Cys	Glu	Thr	Gly
10				15					20					25	
Cys	Cys	Gln	Arg	Ala	Pro	Asp	Asn	Cys	Glu	Ser	His	Cys	Ala	Glu	Lys
			30				35						40		
Gly	Ser	Glu	Gly	Ser	Leu	Cys	Gln	Thr	Gln	Val	Phe	Phe	Gly	Gln	Tyr
		45					50						55		
Arg	Ala	Cys	Pro	Cys	Leu	Arg	Asn	Leu	Thr	Cys	Ile	Tyr	Ser	Lys	Asn
	60					65						70			
Glu	Lys	Trp	Leu	Ser	Ile	Ala	Tyr	Gly	Arg	Cys	Gln	Lys	Ile	Gly	Arg
	75				80						85				
Gln	Lys	Leu	Ala	Lys	Lys	Met	Phe	Phe							
90					95										

<210> 180

<211> 59

<212> PRT

<213> Homo sapiens

<400> 180

Met	Ile	Leu	Cys	Phe	Leu	Leu	Pro	His	His	Arg	Leu	Gln	Glu	Ala	Arg
1			5					10						15	
Gln	Ile	Gln	Val	Leu	Lys	Met	Leu	Pro	Arg	Glu	Lys	Leu	Arg	Arg	Arg
		20					25					30			
Glu	Glu	Arg	Lys	Gln	Ile	Asn	Gly	Lys	Lys	Glu	Arg	Thr	Lys	Tyr	Glu
	35					40						45			
Thr	Pro	Arg	Lys	Arg	Glu	Gly	Lys	Lys	Lys	Lys					
	50					55									

<210> 181

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 181

Met	Val	Ala	Leu	Asn	Leu	Ile	Leu	Val	Pro	Cys	Cys	Ala	Ala	Trp	Cys
			-10					-5						1	
Asp	Pro	Arg	Arg	Ile	His	Ser	Gln	Asp	Asp	Val	Pro	Arg	Ser	Ser	Ala
	5					10					15				
Ala	Asp	Thr	Gly	Ser	Ala	Met	Gln	Arg	Arg	Glu	Ala	Trp	Ala	Gly	Trp
	20				25					30					
Arg	Arg	Ser	Gln	Pro	Phe	Ser	Val	Gly	Leu	Pro	Ser	Ala	Glu	Arg	Leu
35				40				45					50		
Glu	Asn	Gln	Pro	Gly	Lys	Leu	Ser	Trp	Arg	Ser	Leu	Val	Gly	Glu	Gly
			55					60					65		
Tyr	Arg	Ile	Cys	Asp	Leu										

<210> 182
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

<400> 182
 Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
 -55 -50 -45
 Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
 -40 -35 -30
 Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
 -25 -20 -15
 Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
 -10 -5 1 5
 Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
 10 15 20
 Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg
 25 30 35
 Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly
 40 45 50
 Gln Gln Glu Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu
 55 60 65 70
 Ser Leu Gln Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu
 75 80 85
 Leu Arg Ala Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys
 90 95 100
 Leu His Pro Trp Ala
 105

<210> 183
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 183
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
 -35 -30 -25 -20
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
 -15 -10 -5
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
 1 5 10
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
 15 20 25
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 30 35 40 45

<210> 184

<211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 184
 Met Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu
 -20 -15 -10
 Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile
 -5 1 5 10
 Lys Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Cys
 15 20 25
 Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys Ile Cys Cys Ser Ala Phe
 30 35 40
 Cys Gly Asn Ile Cys Met Ser Ile Leu
 45 50

<210> 185
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 185
 Met Leu Gly Ala Glu Thr Glu Glu Lys Leu Phe Asp Ala Pro Leu Ser
 1 5 10 15
 Ile Ser Lys Arg Glu Gln Leu Glu Gln Gln Val Pro Glu Asn Tyr Phe
 20 25 30
 Tyr Val Pro Asp Leu Gly Gln Val Pro Glu Ile Asp Val Pro Ser Tyr
 35 40 45
 Leu Pro Asp Leu Pro Gly Ile Ala Asn Asp Leu Met Tyr Ile Ala Asp
 50 55 60
 Leu Gly Pro Gly Ile Ala Pro Ser Ala Pro Gly Thr Ile Pro Glu Leu
 65 70 75 80
 Pro Thr Phe His Thr Glu Val Ala Glu Pro Leu Lys Thr Tyr Lys Met
 85 90 95
 Gly Tyr

<210> 186
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 186
 Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu
 -20 -15 -10
 Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val
 -5 1 5 10
 Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val
 15 20 25
 Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro

<400> 189

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala
		-40					-35					-30			
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe
	-25					-20					-15				
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Pro	Ile	Ile
-10					-5					1				5	
Leu	Gln	Glu	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser
			10					15					20		
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys
		25					30					35			
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met
	40					45					50				
Glu	Gln	Cys	Gln	Lys	Lys	Pro	Glu	Asn	Ser	Ala	Glu	Ser	Asn	Thr	Glu
55					60					65					70
Glu	Thr	Lys	Arg	Thr	Asp	Leu	Thr	Gln	Asp	Asp	Leu	His	Leu	Lys	Ile
				75					80					85	
Leu	Lys	Asp	Ile	Leu	Cys	Glu	Phe	Leu	Ser	Asn	Ile	Phe	Gln	Ala	Leu
			90					95					100		
Thr	Lys	Glu	Thr	Val	Ala	Gln	Gly	Val	Lys	Glu	Gly	Gln	Leu	Ser	Lys
		105					110					115			
Gln	Lys	Cys	Ser	Ser	Ala	Phe	Gln	Asn	Leu	Leu	Pro	Phe	Tyr	Ser	Pro
	120					125					130				
Val	Val	Glu	Asp	Phe	Ile	Lys	Ile	Leu	Arg	Glu	Val	Asp	Lys	Ala	Leu
135					140					145					150
Ala	Asp	Asp	Leu	Glu	Lys	Asn	Phe	Pro	Ser	Leu	Lys	Val	Gln	Thr	
				155					160					165	

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<210> 190
<211> 201
<212> PRT
<213> Homo sapiens
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<400> 190

Met	Gln	Val	Ala	Leu	Lys	Glu	Asp	Leu	Asp	Ala	Leu	Lys	Glu	Lys	Phe
1				5					10					15	
Arg	Thr	Met	Glu	Ser	Asn	Gln	Lys	Ser	Ser	Phe	Gln	Glu	Ile	Pro	Lys
			20					25					30		
Leu	Asn	Glu	Glu	Leu	Leu	Ser	Lys	Gln	Lys	Gln	Leu	Glu	Lys	Ile	Glu
			35				40					45			
Ser	Gly	Glu	Met	Gly	Leu	Asn	Lys	Val	Trp	Ile	Asn	Ile	Thr	Glu	Met
			50				55				60				
Asn	Lys	Gln	Ile	Ser	Leu	Leu	Thr	Ser	Ala	Val	Asn	His	Leu	Lys	Ala
65					70					75					80
Asn	Val	Lys	Ser	Ala	Ala	Asp	Leu	Ile	Ser	Leu	Pro	Thr	Thr	Val	Glu
				85					90					95	
Gly	Leu	Gln	Lys	Ser	Val	Ala	Ser	Ile	Gly	Asn	Thr	Leu	Asn	Ser	Val
			100					105					110		
His	Leu	Ala	Val	Glu	Ala	Leu	Gln	Lys	Thr	Val	Asp	Glu	His	Lys	Lys
			115				120					125			
Thr	Met	Glu	Leu	Leu	Gln	Ser	Asp	Met	Asn	Gln	His	Phe	Leu	Lys	Glu
			130			135					140				
Thr	Pro	Gly	Ser	Asn	Gln	Ile	Ile	Pro	Ser	Pro	Ser	Ala	Thr	Ser	Glu

145					150					155				160
Leu	Asp	Asn	Lys	Thr	His	Ser	Glu	Asn	Leu	Lys	Gln	Met	Gly	Asp
				165					170					175
Ser	Ala	Thr	Leu	Lys	Arg	Gln	Ser	Leu	Asp	Gln	Val	Thr	Asn	Arg
			180					185					190	
Asp	Thr	Val	Lys	Ile	Gln	Lys	Lys	Lys						
		195					200							

<210> 191
 <211> 379
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 191

Met	Pro	His	Ser	Ser	Leu	His	Pro	Ser	Ile	Pro	Cys	Pro	Arg	Gly	His
		-35					-30					-25			
Gly	Ala	Gln	Lys	Ala	Ala	Leu	Val	Leu	Leu	Ser	Ala	Cys	Leu	Val	Thr
	-20					-15					-10				
Leu	Trp	Gly	Leu	Gly	Glu	Pro	Pro	Glu	His	Thr	Leu	Arg	Tyr	Leu	Val
-5					1			5						10	
Leu	His	Leu	Ala	Ser	Leu	Gln	Leu	Gly	Leu	Leu	Leu	Asn	Gly	Val	Cys
			15					20					25		
Ser	Leu	Ala	Glu	Glu	Leu	Arg	His	Ile	His	Ser	Arg	Tyr	Arg	Gly	Ser
	30					35						40			
Tyr	Trp	Arg	Thr	Val	Arg	Ala	Cys	Leu	Gly	Cys	Pro	Leu	Arg	Arg	Gly
45					50					55					
Ala	Leu	Leu	Leu	Leu	Ser	Ile	Tyr	Phe	Tyr	Tyr	Ser	Leu	Pro	Asn	Ala
60					65					70					75
Val	Gly	Pro	Pro	Phe	Thr	Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	Gln
				80				85					90		
Ala	Leu	Asn	Ile	Leu	Leu	Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	Ile
		95					100					105			
Ser	Ala	Val	Cys	Glu	Lys	Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	Ala
	110					115					120				
Trp	Ser	Tyr	Tyr	Ile	Gly	Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln
	125				130					135					
Ala	Arg	Ile	Arg	Thr	Tyr	Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly
140				145					150						155
Ala	Val	Ser	Gln	Arg	Leu	Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val
			160					165					170		
Pro	Asp	Asn	Leu	Ser	Met	Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys
		175					180					185			
Leu	Pro	Gln	Gln	Thr	Gly	Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr
	190				195						200				
Ser	Asn	Ser	Ile	Tyr	Glu	Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr
	205				210				215						
Cys	Val	Leu	Glu	Tyr	Ala	Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser
220				225					230						235
Gln	Tyr	Ser	Gln	Ala	Gly	Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala
			240					245					250		
Lys	Leu	Phe	Cys	Arg	Thr	Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu
		255					260					265			
Ser	Gln	Asn	Asn	Cys	Arg	Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp

270 275 280
 Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
 285 290 295
 Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
 300 305 310 315
 Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Leu Ser Gly Met
 320 325 330
 Gly Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 335 340

<210> 192
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 192
 Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
 1 5 10 15
 Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
 20 25 30
 Glu Asp Val Leu Glu Glu Cys Met Ser Leu Pro Lys Leu Ser Ser Tyr
 35 40 45
 Ser Gly Trp Val Val Glu His Val Leu Pro His Met Gln Glu Asn Gln
 50 55 60
 Pro Leu Ser Glu Thr Ser Pro Ser Ser Thr Ser Ala Ser Ala Leu Asp
 65 70 75 80
 Gln Pro Ser Phe Val Pro Lys Ser Pro Asp Ala Ser Ser Ala Phe Ser
 85 90 95
 Pro Ala Ser Pro Ala Thr Pro Asn Gly Thr Lys Gly Lys Lys Lys Lys
 100 105 110

<210> 193
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 193
 Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly Ser
 1 5 10 15
 Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg Asn
 20 25 30
 Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
 35 40

<210> 194
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 194
 Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu

1		5		10		15									
Cys	Leu	Pro	Cys	Leu	Ser	Trp	Asn	Lys	Lys	Gly	Asn	Val	Leu	Gln	Leu
		20						25					30		
Pro	Asn	Phe													
		35													

<210> 195
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 195
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
-15 -10 -5
Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Gln Ala Ser
1 5 10
Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile
15 20 25 30
Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys
35 40 45
Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala Asp
50 55 60
Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly
65 70 75
Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala
80 85 90
Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe
95 100 105 110
Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr
115 120 125
Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn Pro
130 135 140
Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser Gln
145 150 155
Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly Asp
160 165 170
Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys Pro
175 180 185 190
His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu Val
195 200 205
Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile Gly
210 215 220
Arg Thr Ala Trp
225

<210> 196
 <211> 353
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 196

Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
-30 -25 -20
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
-15 -10 -5
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln
1 5 10
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp
15 20 25 30
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn
35 40 45
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys
50 55 60
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr
65 70 75
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr
80 85 90
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly
95 100 105 110
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met
115 120 125
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
130 135 140
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
145 150 155
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
160 165 170
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
175 180 185 190
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
195 200 205
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala
210 215 220
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
225 230 235
Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
240 245 250
Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
255 260 265 270
Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
275 280 285
Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
290 295 300
Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
305 310 315
Leu

<210> 197

<211> 30

<212> PRT

<213> Homo sapiens

<400> 197

Met Gln Met Asp Thr Phe Phe Met Ser Glu Lys His Thr His Thr His
1 5 10 15
Thr His Ile His Thr His Thr Arg Lys Thr Lys Lys Lys Lys

20

25

30

<210> 198

<211> 112

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48..-1

<400> 198

Met	Gln	Asp	Thr	Gly	Ser	Val	Val	Pro	Leu	His	Trp	Phe	Gly	Phe	Gly
				-45				-40					-35		
Tyr	Ala	Ala	Leu	Val	Ala	Ser	Gly	Gly	Ile	Ile	Gly	Tyr	Val	Lys	Ala
		-30					-25					-20			
Gly	Ser	Val	Pro	Ser	Leu	Ala	Ala	Gly	Leu	Leu	Phe	Gly	Ser	Leu	Ala
		-15				-10					-5				
Gly	Leu	Gly	Ala	Tyr	Gln	Leu	Ser	Gln	Asp	Pro	Arg	Asn	Val	Trp	Val
1			5					10					15		
Phe	Leu	Ala	Thr	Ser	Gly	Thr	Leu	Ala	Gly	Ile	Met	Gly	Met	Arg	Phe
		20						25				30			
Tyr	His	Ser	Gly	Lys	Phe	Met	Pro	Ala	Gly	Leu	Ile	Ala	Gly	Ala	Ser
		35					40				45				
Leu	Leu	Met	Val	Ala	Lys	Val	Gly	Val	Ser	Met	Phe	Asn	Arg	Pro	His
	50					55					60				

<210> 199

<211> 54

<212> PRT

<213> Homo sapiens

<400> 199

Glu	Ile	Ala	Gly	Tyr	Gly	Ala	Glu	Gly	Phe	Ser	Ser	Val	Leu	Gly	Tyr
1			5					10					15		
Pro	Arg	Trp	His	Arg	Leu	Pro	Pro	Gln	Ser	Leu	Gln	His	His	Gln	Tyr
		20						25				30			
Cys	Gln	Arg	Arg	Trp	Pro	Asp	Arg	Arg	Cys	Leu	Gln	Ser	His	Thr	Gln
	35					40					45				
Ser	Ser	Gly	His	Leu	Pro										
	50														

<210> 200

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<220>

<221> UNSURE

<222> -14,46

<223> Xaa = any one of the twenty amino acids

<400> 200

Met	Ala	Ala	Ser	Thr	Ser	Met	Xaa	Pro	Val	Ala	Val	Thr	Ala	Ala	Val
-20						-15					-10				
Ala	Pro	Val	Leu	Ser	Ile	Asn	Ser	Asp	Phe	Ser	Asp	Leu	Arg	Glu	Ile
-5					1			5						10	
Lys	Lys	Gln	Leu	Leu	Leu	Ile	Ala	Gly	Leu	Thr	Arg	Glu	Arg	Gly	Leu
		15						20					25		
Leu	His	Ser	Ser	Lys	Trp	Ser	Ala	Glu	Leu	Ala	Phe	Ser	Leu	Pro	Ala
	30						35					40			
Leu	Pro	Xaa	Gly	Gln	Leu	Gln	Pro	Pro	Pro	Pro	Ile	Thr	Glu	Glu	Asp
45						50					55				
Ala	Gln	Asp	Met	Asp	Ala	Tyr	Thr	Leu	Ala	Lys	Ala	Tyr	Phe	Asp	Val
60					65					70					75
Lys	Glu	Tyr	Asp	Arg	Ala	Ala	His	Phe	Leu	His	Gly	Cys	Asn	Ser	Lys
			80					85						90	
Lys	Ala	Tyr	Phe	Leu	Tyr	Met	Tyr	Ser	Arg	Tyr	Leu	Val	Arg	Ala	Ile
		95					100						105		
Leu	Lys	Cys	His	Ser	Ala	Phe	Ser	Glu	Thr	Ser	Ile	Phe	Arg	Thr	Asn
	110						115						120		
Gly	Lys	Val	Lys	Ser	Phe	Lys									
125						130									

<210> 201

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 201

Met	Ser	Met	Ala	Val	Glu	Thr	Phe	Gly	Phe	Phe	Met	Ala	Thr	Val	Gly
-25					-20				-15						-10
Leu	Leu	Met	Leu	Gly	Val	Thr	Leu	Pro	Asn	Ser	Tyr	Trp	Arg	Val	Ser
			-5					1				5			
Thr	Val	His	Gly	Asn	Val	Ile	Thr	Asn	Thr	Ile	Phe	Glu	Asn	Leu	
	10					15					20				
Trp	Phe	Ser	Cys	Ala	Thr	Asp	Ser	Leu	Gly	Val	Tyr	Asn	Cys	Trp	Glu
25					30					35					
Phe	Pro	Ser	Met	Leu	Ala	Leu	Ser	Gly	Tyr	Ile	Gln	Ala	Cys	Arg	Ala
40					45				50						55
Leu	Met	Ile	Thr	Ala	Ile	Leu	Leu	Gly	Phe	Leu	Gly	Leu	Leu	Leu	Gly
			60					65						70	
Ile	Ala	Gly	Leu	Arg	Cys	Thr	Asn	Ile	Gly	Gly	Leu	Glu	Leu	Ser	Arg
		75					80					85			
Lys	Ala	Lys	Leu	Ala	Ala	Thr	Ala	Gly	Ala	Pro	His	Ile	Leu	Ala	Gly
	90					95					100				
Ile	Cys	Gly	Met	Val	Ala	Ile	Ser	Trp	Tyr	Ala	Phe	Asn	Ile	Thr	Arg
	105					110				115					
Asp	Phe	Phe	Asp	Pro	Leu	Tyr	Pro	Gly	Thr	Lys	Tyr	Glu	Leu	Gly	Pro
120					125				130						135
Ala	Leu	Tyr	Leu	Gly	Trp	Ser	Ala	Ser	Leu	Ile	Ser	Ile	Leu	Gly	Gly
			140					145					150		
Leu	Cys	Leu	Cys	Ser	Ala	Cys	Cys	Cys	Gly	Ser	Asp	Glu	Asp	Pro	Ala
	155						160					165			
Ala	Ser	Ala	Arg	Arg	Pro	Tyr	Gln	Ala	Pro	Val	Ser	Val	Met	Pro	Val
	170						175					180			

Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg
 185 190 195
 Asn Ala Tyr Val
 200

<210> 202
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 202
 Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
 -45 -40 -35
 Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
 -30 -25 -20
 Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
 -15 -10 -5 1
 Pro Asp Leu Pro Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
 5 10 15

<210> 203
 <211> 146
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 203
 Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly
 -30 -25 -20
 Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile
 -15 -10 -5 1
 Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys
 5 10 15
 Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu
 20 25 30
 Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn
 35 40 45
 Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile Pro Val Ser Gly Ser
 50 55 60 65
 Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser Arg Gly Gly Pro Phe
 70 75 80
 Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu Lys Asp Gly Gln
 85 90 95
 Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly Asp Glu Val Lys
 100 105 110
 Lys Glu
 115

<210> 204
 <211> 87

<212> PRT
 <213> Homo sapiens

<400> 204

```

Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser Leu
1          5          10          15
Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His Leu
          20          25          30
Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro Glu
          35          40          45
Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln Ser
          50          55          60
Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu Leu
65          70          75          80
Glu Val Asp Asp Trp Glu Phe
          85
  
```

<210> 205
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 205

```

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
          -25          -20          -15
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
          -10          -5          1          5
Leu Ser Leu Arg Ser Ala Met Ser
          10
  
```

<210> 206
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 206

```

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
1          5          10          15
Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
          20          25          30
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
          35          40          45
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
          50          55          60
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
65          70          75          80
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
          85          90          95
Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val
          100          105          110
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
          115          120          125
His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
  
```

130 135 140
 Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
 145 150

 <210> 207
 <211> 101
 <212> PRT
 <213> Homo sapiens

 <400> 207
 Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
 1 5 10 15
 Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
 20 25 30
 Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
 35 40 45
 Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
 50 55 60
 Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
 65 70 75 80
 Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
 85 90 95
 Lys Gln Thr Ser Val
 100

<210> 208
 <211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 208
 Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly
 -20 -15 -10
 Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn
 -5 1 5 10
 Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg Ala Leu Glu
 15 20 25
 Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile Ser Asp Ser
 30 35 40
 Glu Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys Lys Ala Ser
 45 50 55
 Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys Lys Lys Cys
 60 65 70
 Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Glu Val Glu Arg
 75 80 85 90
 Lys Lys Lys Cys His Lys Gln Ala Leu Val Gly Ser Asp Ser Ala Glu
 95 100 105
 Asp Glu Lys Arg Lys Arg Lys Cys Gln Lys His Ala Pro Ile Asn Ser
 110 115 120
 Ala Gln His Leu Asp Asn Val Asp Gln Thr Gly Pro Lys Ala Trp Lys
 125 130 135
 Gly Ser Thr Thr Asn Asp Pro Pro Lys Gln Ser Pro Gly Ser Thr Ser
 140 145 150

Pro Lys Pro Pro His Thr Leu Ser Arg Lys Gln Trp Arg Asn Arg Gln
 155 160 165 170
 Lys Asn Lys Arg Arg Cys Lys Asn Lys Phe Gln Pro Pro Gln Val Pro
 175 180 185
 Asp Gln Ala Pro Ala Glu Ala Pro Thr Glu Lys Thr Glu Val Ser Pro
 190 195 200
 Val Pro Arg Thr Asp Ser His Gly Ala Arg Ala Gly Ala Leu Arg Ala
 205 210 215
 Arg Met Ala Gln Arg Leu Asp Gly Ala Arg Phe Arg Tyr Leu Asn Glu
 220 225 230
 Gln Leu Tyr Ser Gly Pro Ser Ser Ala Ala Gln Arg Leu Phe Gln Glu
 235 240 245 250
 Asp Pro Glu Ala Phe Leu Leu Tyr His Arg Gly Phe Gln Ser Gln Val
 255 260 265
 Lys Lys Trp Pro Leu Gln Pro Val Asp Arg Ile Ala Arg Asp Leu Arg
 270 275 280
 Gln Arg Pro Ala Ser Leu Val Val Ala Asp Phe Gly Cys Gly Asp Cys
 285 290 295
 Arg Leu Ala Ser Ser Ile Arg Asn Pro Val His Cys Phe Asp Leu Ala
 300 305 310
 Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln Val Pro Leu
 315 320 325 330
 Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser Leu Met Gly
 335 340 345
 Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val Leu Lys Pro
 350 355 360
 Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe Glu Asp Val
 365 370 375
 Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys Ile Val Ser
 380 385 390
 Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe Gln Lys Thr
 395 400 405 410
 Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly Leu Gln Leu
 415 420 425
 Gln Pro Cys Leu Tyr Lys Arg Arg
 430

<210> 209

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 209

Met Pro Ser Ser Phe Phe Leu Leu Leu Gln Phe Phe Leu Arg Ile Asp
 -15 -10 -5
 Gly Val Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp
 1 5 10 15
 Lys Thr Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser
 20 25 30
 Ser Leu Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile
 35 40 45
 Ser Gln Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe
 50 55 60

Pro Glu Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln
65 70 75
Val Glu
80

<210> 210
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29...-1

<400> 210
Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu
-25 -20 -15
Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe
-10 -5 1
Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr
5 10 15
Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro
20 25 30 35
Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg
40 45 50
Asn Ala Ser

<210> 211
<211> 229
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 211
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
30 35 40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
45 50 55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
60 65 70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
75 80 85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
90 95 100 105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
110 115 120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
125 130 135

Ser Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
 140 145 150
 Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
 155 160 165
 Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
 170 175 180 185
 Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
 190 195 200
 Arg Lys Ser Arg Thr
 205

<210> 212
 <211> 152
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 212
 Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
 -20 -15 -10
 Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
 -5 1 5 10
 Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly
 15 20 25
 Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr
 30 35 40
 Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly
 45 50 55
 Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val
 60 65 70 75
 Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp
 80 85 90
 Lys Ala Leu Ile Phe Asn Lys Ile His His Glu Leu Asn Gln Phe Cys
 95 100 105
 Ser Val His Thr Leu Gln Glu Val Tyr Ile Glu Leu Phe Gly Leu Glu
 110 115 120
 Asn Asp Phe Ser Gln Glu Ser Ser
 125 130

<210> 213
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 213
 Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
 -50 -45 -40
 Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
 -35 -30 -25
 Ala Thr Pro Ser Ala Arg Ala Ala Ala Val Val Ala Ala Ala Ala

-20	-15	-10
Arg Thr Gly Ser Glu Ala	Arg Val Ser Lys Ala Ala	Leu Ala Thr Lys
-5	1	5
Leu Leu Ser Leu Ser Gly Val	Phe Ala Val His Lys Pro	Lys Gly Pro
15	20	25
Thr Ser Ala Glu Leu Leu Asn Arg	Leu Lys Glu Lys Leu Leu Ala Glu	
30	35	40
Ala Gly Met Pro Ser Pro Glu Trp	Thr Lys Arg Lys Lys Gln Thr Leu	
45	50	55
Lys Ile Gly His Gly Gly Thr Leu	Asp Ser Ala Ala Arg Gly Val Leu	
60	65	70
Val Val Gly Ile Gly Ser Gly Thr	Lys Met Leu Thr Ser Met Leu Ser	
75	80	85
Gly Ser Lys Arg Tyr Thr Ala Ile	Gly Glu Leu Gly Lys Ala Thr Asp	
95	100	105
Thr Leu Asp Ser Thr Gly Lys Val	Thr Glu Glu Lys Pro Tyr Gly Met	
110	115	120
Asn Leu Ile		
125		

<210> 214
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -92..-1

<400> 214
Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu
-90 -85 -80
Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro
-75 -70 -65
Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp
-60 -55 -50 -45
Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr
-40 -35 -30
Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala
-25 -20 -15
Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val
-10 -5 1
Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val
5 10 15 20
Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr Phe
25 30 35
Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu Cys
40 45 50
His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu Thr
55 60 65
Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn
70 75 80
Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala
85 90 95 100
Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln
105 110 115
Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys Leu

		120						125				130			
His	Gln	Gln	Leu	Glu	Val	Ile	Pro	Gly	Tyr	Glu	Glu	Leu	Leu	Ala	Asp
		135						140				145			
Ile	Val	Asn	Ile	Cys	Val	Asp	Tyr	Tyr	Glu	Asn	Lys	Met	Tyr	Leu	Thr
		150				155					160				
Pro	Ser	Glu	Lys	His	Met	Leu	Leu	Lys	Val	Lys	Leu	Pro			
165					170				175						

<210> 215
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 215															
Met	Gln	Thr	Val	Tyr	Tyr	Gly	Ser	Leu	Gly	Leu	Trp	Leu	Ala	Leu	Val
		-20					-15				-10				
Asp	Gly	Leu	Val	Arg	Ser	Ser	Pro	Ser	Leu	Asp	Gln	Met	Phe	Asp	Ala
	-5				1				5					10	
Glu	Ile	Leu	Gly	Phe	Ser	Thr	Pro	Pro	Gly	Arg	Leu	Ser	Met	Met	Ser
			15						20				25		
Phe	Ile	Phe	Asn	Ala	Leu	Thr	Cys	Ala	Leu	Gly	Leu	Leu	Tyr	Phe	Ile
		30					35					40			
Arg	Arg	Gly	Lys	Gln	Cys	Leu	Asp	Phe	Thr	Val	Thr	Val	His	Phe	Phe
	45						50				55				
His	Leu	Leu	Gly	Cys	Trp	Phe	Tyr	Ser	Ser	Arg	Phe	Pro	Ser	Ala	Leu
	60				65					70					
Thr	Trp	Trp	Leu	Val	Gln	Ala	Val	Cys	Ile	Ala	Leu	Met	Ala	Val	Ile
	75			80					85					90	
Gly	Glu	Tyr	Leu	Cys	Met	Arg	Thr	Glu	Leu	Lys	Glu	Ile	Pro	Leu	Asn
			95					100					105		
Ser	Ala	Pro	Lys	Ser	Asn	Val									
			110												

<210> 216
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 216															
Met	Asn	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe	Ser
		-35					-30					-25			
Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Val	Phe	Ala	Leu	Val	Thr
		-20				-15				-10					
Ala	Val	Cys	Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu
	-5			1				5						10	
Phe	Asn	Pro	Asn	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys
			15				20						25		
Glu	Val	Leu													

<210> 217
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 217
 Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
 -50 -45 -40
 Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
 -35 -30 -25
 Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
 -20 -15 -10
 Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
 -5 1 5 10
 Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
 15 20 25
 Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
 30 35 40
 Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
 45 50 55
 Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr
 60 65 70

<210> 218
 <211> 376
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 218
 Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
 -20 -15 -10
 Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
 -5 1 5 10
 Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg Ile Gly
 15 20 25
 Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys Ala Leu
 30 35 40
 Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg Thr Arg
 45 50 55
 Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val Gly Gly
 60 65 70 75
 Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg Ser Phe
 80 85 90
 Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln Thr Lys
 95 100 105
 Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys Leu Leu
 110 115 120
 Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly Thr Leu
 125 130 135

Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala Val Asp
 140 145 150 155
 Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala Leu Thr
 160 165 170
 Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp Asn His
 175 180 185
 Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp Leu Val
 190 195 200
 Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser Trp Leu
 205 210 215
 Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe Gln Val
 220 225 230 235
 Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys Pro Trp
 240 245 250
 Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro Val Ala
 255 260 265
 Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg Ile Gln
 270 275 280
 Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro Leu Pro
 285 290 295
 Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val Ser Gly
 300 305 310 315
 Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly Gly His
 320 325 330
 Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu Ala Gln
 335 340 345
 Arg Ser Tyr Leu Pro Gln Ile Ser
 350 355

<210> 219

<211> 211

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30..-1

<400> 219

Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 -30 -25 -20 -15
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 -10 -5 1
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 5 10 15
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 20 25 30
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 35 40 45 50
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 55 60 65
 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val Pro Arg Met
 70 75 80
 Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe
 85 90 95
 His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro
 100 105 110

Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser
 115 120 125 130
 Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly
 135 140 145
 Thr His Lys Asp Val Leu Glu Gly Thr Glu Ser Ser Ser His Ser
 150 155 160
 Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser
 165 170 175
 Arg Gln Leu
 180

<210> 220
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 220
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
 -60 -55 -50 -45
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
 -40 -35 -30
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
 -25 -20 -15
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
 -10 -5 1
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
 5 10 15 20
 Ala Leu Leu Arg Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu
 25 30 35
 Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
 40 45 50
 Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe
 55 60 65
 Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
 70 75 80
 Pro Glu Phe His Ile Glu Ile Leu Ser Ile
 85 90

<210> 221
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 221
 Met Lys Gly Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala
 -40 -35 -30
 Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro
 -25 -20 -15
 Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met

-10					-5					1				5	
Lys	Ser	Ser	Gln	Ala	Ala	Arg	Lys	Asp	Asp	Phe	Leu	Arg	Ser	Leu	Ser
			10					15					20		
Asp	Gly	Asp	Ser	Gly	Thr	Ser	Glu	His	Ile	Ser	Ala	Val	Val	Thr	Ser
		25					30					35			
Pro	Arg	Ile	Ser	Cys	His	Gly	Ala	Ala	Ile	Pro	Thr	Ala	Arg	Ala	Leu
		40				45					50				
Cys	Leu	Gly	Cys	Ser	Cys	Cys	Thr	Glu	Arg	Leu	Leu	Leu	Pro	Pro	Pro
55					60					65					70
Ser	Leu	Leu	Ser	Leu	Glu	Ala	Pro	Ala	Ser	Thr					
				75					80						

<210> 222

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 222

Met	Ala	Met	Ala	Gln	Lys	Leu	Ser	His	Leu	Leu	Pro	Ser	Leu	Arg	Gln
				-15					-10					-5	
Val	Ile	Gln	Glu	Pro	Gln	Leu	Ser	Leu	Gln	Pro	Glu	Pro	Val	Phe	Thr
			1				5					10			
Val	Asp	Arg	Ala	Glu	Val	Pro	Pro	Leu	Phe	Trp	Lys	Pro	Tyr	Ile	Tyr
	15					20					25				
Ala	Gly	Tyr	Arg	Pro	Leu	His	Gln	Thr	Trp	Arg	Phe	Tyr	Phe	Arg	Thr
30					35				40					45	
Leu	Phe	Gln	Gln	His	Asn	Glu	Ala	Val	Asn	Val	Trp	Thr	His	Leu	Leu
				50					55					60	
Ala	Ala	Leu	Val	Leu	Leu	Leu	Arg	Leu	Ala	Leu	Phe	Val	Glu	Thr	Val
			65				70					75			
Asp	Phe	Trp	Gly	Asp	Pro	His	Ala	Leu	Pro	Leu	Phe	Ile	Ile	Val	Leu
	80					85					90				
Ala	Ser	Phe	Thr	Tyr	Leu	Ser	Leu	Ser	Ala	Leu	Ala	His	Leu	Leu	Gln
	95				100					105					
Ala	Lys	Ser	Glu	Phe	Trp	His	Tyr	Ser	Phe	Phe	Phe	Leu	Asp	Tyr	Val
110					115					120					125
Gly	Val	Ala	Val	Tyr	Gln	Phe	Gly	Ser	Ala	Leu	Ala	His	Phe	Tyr	Tyr
				130					135					140	
Ala	Ile	Glu	Pro	Ala	Trp	His	Ala	Gln	Val	Gln	Ala	Val	Phe	Leu	Pro
			145				150					155			
Met	Ala	Ala	Phe	Leu	Ala	Trp	Leu	Ser	Cys	Ile	Gly	Ser	Cys	Tyr	Asn
	160					165						170			
Lys	Tyr	Ile	Gln	Lys	Pro	Gly	Leu	Leu	Gly	Arg	Thr	Cys	Gln	Glu	Val
	175				180					185					
Pro	Ser	Val	Leu	Ala	Tyr	Ala	Leu	Asp	Ile	Ser	Pro	Val	Val	His	Arg
190					195					200				205	
Ile	Phe	Val	Ser	Ser	Asp	Pro	Thr	Thr	Asp	Asp	Pro	Ala	Leu	Leu	Tyr
				210					215					220	
His	Lys	Cys	Gln	Val	Val	Phe	Phe	Leu	Leu	Ala	Ala	Ala	Phe	Phe	Ser
			225				230					235			
Thr	Phe	Met	Pro	Glu	Arg	Trp	Phe	Pro	Gly	Ser	Cys	His	Val	Phe	Gly
	240					245					250				
Gln	Gly	His	Gln	Leu	Phe	His	Ile	Phe	Leu	Val	Leu	Cys	Thr	Leu	Ala

255		260		265
Gln Leu Glu Ala Val	Ala Leu Asp Tyr Glu	Ala Arg Arg Pro Ile Tyr		
270	275	280		285
Glu Pro Leu His Thr	His Trp Pro His Asn	Phe Ser Gly Leu Phe Leu		
	290	295		300
Leu Thr Val Gly Ser Ser	Ile Leu Thr Ala Phe	Leu Leu Ser Gln Leu		
	305	310		315
Val Gln Arg Lys Leu Asp	Gln Lys Thr Lys			
	320	325		

<210> 223
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 223
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20 -15 -10 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
1 5 10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
15 20 25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
30 35 40
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
45 50 55 60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
65 70 75
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
80 85 90
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
95 100 105
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
110 115 120
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
125 130 135 140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
145 150 155
His Leu Leu Ala Val Thr Lys Glu Ser Met Leu Pro Ala Gly Ala Glu
160 165 170
Ser Lys His Thr Ala Thr Pro Ala His Ala Cys Val Gln Thr Gly Lys
175 180 185
Pro Lys
190

<210> 224
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 224

Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20 -15 -10 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
1 5 10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
15 20 25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
30 35 40
Asn Asp Ala Pro Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
45 50 55 60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
65 70 75
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
80 85 90
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
95 100 105
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
110 115 120
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
125 130 135 140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
145 150 155
His Leu Leu Ala Asp Thr Met Leu
160

<210> 225

<211> 227

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22...-1

<400> 225

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
-20 -15 -10
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
-5 1 5 10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
15 20 25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
30 35 40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
45 50 55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
60 65 70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
75 80 85 90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
95 100 105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
110 115 120
Ser Gly Phe His Arg Tyr Gln Phe Val Tyr Leu Gln Glu Gly Lys
125 130 135

Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
140 145 150
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
155 160 165 170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
175 180 185
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
190 195 200
Ala Ala Cys
205

<210> 226
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 226
Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu
-40 -35 -30
Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
-25 -20 -15 -10
Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
-5 1 5
Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile
10 15 20
Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
25 30

<210> 227
<211> 73
<212> PRT
<213> Homo sapiens

<400> 227
Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly
1 5 10 15
Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile
20 25 30
Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met Val Lys Lys Ile Ala
35 40 45
Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val
50 55 60
Asn Leu Leu Glu Val Cys Lys Lys Lys
65 70

<210> 228
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 228

Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
-15 -10 -5
Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp
1 5 10 15
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr
20 25 30
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe
35 40 45
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg
50 55 60
Lys Asn
65

<210> 229

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -56..-1

<400> 229

Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
Ile Leu Ala Lys Lys Lys
60

<210> 230

<211> 54

<212> PRT

<213> Homo sapiens

<400> 230

Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
Gly Arg Gly Arg Pro His
50

<210> 231
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 231
 Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val
 -10 -5 1
 Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr
 5 10 15
 Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
 20 25 30
 Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile
 35 40 45 50
 Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
 55 60 65
 Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met
 70 75 80
 Thr Ala Tyr Leu Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu
 85 90 95
 Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly
 100 105 110
 Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu
 115 120 125 130
 Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile
 135 140 145
 Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg
 150 155 160
 Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp
 165 170 175
 Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys
 180 185 190
 Gln Glu
 195

<210> 232
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95

Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
 100 105

<210> 233
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 233
 Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
 -15 -10 -5
 Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
 1 5 10
 Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
 15 20 25

<210> 234
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg Leu
 1 5 10 15
 Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys Thr
 20 25 30
 Phe Phe Gln Ile
 35

<210> 235
 <211> 307
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 235
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
 -10 -5 1
 Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
 5 10 15
 Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
 20 25 30 35
 Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50
 Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
 55 60 65
 Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
 70 75 80
 Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
 85 90 95

Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys Lys Gly Leu
 100 105 110 115
 Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser
 120 125 130
 Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr
 135 140 145
 Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
 150 155 160
 Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp
 165 170 175
 Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
 180 185 190 195
 Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
 200 205 210
 Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
 215 220 225
 Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
 230 235 240
 Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
 245 250 255
 Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
 260 265 270 275
 Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Ala
 280 285 290
 Lys Lys Lys

<210> 236
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 236
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 237
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -19..-1

<400> 237

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 1 5 10
Gln Leu Ser Asp Lys Val His Asn Asp Ile
 15 20

<210> 238

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 238

Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20 -15 -10 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
 30 35 40
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Gly Arg
45 50 55 60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
 65 70 75
Thr Gly Ile Ser Leu Ile Leu Thr Ser Val Phe Phe Thr Trp Leu Ile
 80 85 90
Ile Asp Lys Thr Thr
 95

<210> 239

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<220>

<221> UNSURE

<222> -19,-18,-16,-15

<223> Xaa = any one of the twenty amino acids

<400> 239

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
 -35 -30 -25
Gln His Xaa Xaa Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile
 -20 -15 -10

Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
 -5 1 5 10
 Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu
 15 20 25
 Ile Ser Arg Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val
 30 35 40
 Cys Asp Cys Val Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn
 45 50 55
 Val Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
 60 65 70 75
 His Asn Ile Asn Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr
 80 85 90
 Phe Asp Pro Glu Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe
 95 100 105
 His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly
 110 115 120
 Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val
 125 130 135
 Ile Gly
 140

<210> 240
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 240
 Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val
 -25 -20 -15
 Val Leu Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser
 -10 -5 1 5
 Met Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe Ile
 10 15 20
 Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr Met Ala
 25 30 35
 Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr
 40 45 50
 Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met Lys Gly
 55 60 65
 Leu Lys Cys Arg Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro
 70 75 80 85
 Tyr Phe Lys Met His Lys Pro Val Thr Met Lys Lys Lys Lys
 90 95

<210> 241
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -115...-1

<400> 241
Met Arg Trp Ser Cys Glu His Leu Val Met Val Trp Ile Asn Ala Phe
-115 -110 -105 -100
Val Met Leu Thr Thr Gln Leu Leu Pro Ser Lys Tyr Cys Asp Leu Leu
-95 -90 -85
His Lys Ser Ala Ala His Leu Gly Lys Trp Gln Lys Leu Glu His Gly
-80 -75 -70
Ser Tyr Ser Asn Ala Pro Gln His Ile Trp Ser Glu Asn Thr Ile Trp
-65 -60 -55
Pro Gln Gly Val Leu Val Arg His Ser Arg Cys Leu Tyr Arg Ala Met
-50 -45 -40
Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg Phe
-35 -30 -25 -20
Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu Asn Leu Leu Ile Leu
-15 -10 -5
Ile Glu Gly Gly Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg Ser
1 5 10
Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys Asn
15 20 25
Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Ile Val Leu Gly Arg
30 35 40 45
Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn
50 55

<210> 242
<211> 896
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..173

<220>
<221> sig_peptide
<222> 18..77
<223> Von Heijne matrix
score 6.5
seq GLCVLQLTTAVTS/AF

<220>
<221> polyA_signal
<222> 864..869

<220>
<221> polyA_site
<222> 882..893

<400> 242
aaccttcaca gtgtgag atg cct agt gtg aac agt gct gga tta tgt gtc 50
Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val
-20 -15 -10
ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg 98
Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
-5 1 5
aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc 146
Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala

10	15	20	
cat cat ttc att cat cct tgc ctg gat tgagacgtgt	tccctgattca		193
His His Phe Ile His Pro Cys Leu Asp			
25	30		
aagtgttacc tcaagaagca gaagaagaaa acagactcct	gatagttcag gatgcttcag		253
agagggcagc acttatacct ggtgggtcttt ctgatgggtca	gtttttattcc cctcctgaat		313
ccgaagcagg atctgaagaa gctgaagaaa aacaggacag	tgagaaacca cttttagaac		373
tatgagtact acttttggtta aatgtgaaaa accctcacag	aaagtcacg aggcaaaaag		433
aggcaggcag tggagtctcc ctgtcgacag taaagttgaa	atgggtgacgt ccaactgctgg		493
ctttattgaa cagctaataa agattttattt attgtaatac	ctcacagacg ttgtaccata		553
tccatgcaca tttagttgcc tgcctgtggc tggtaaggta	atgtcatgat tcatcctctc		613
ttcagtgaga ctgagcctga tgtgttaaca aataggtgaa	gaaagtcttg tgctgtattc		673
ctaatacaaaa gacttaatat attgaagtaa cactttttta	gtaagcaaga taccttttta		733
tttcaattca cagaatggaa tttttttggt tcatgtctca	gattttatttt gtatttcctt		793
tttaacactc tacatttccc ttgtttttta actcatgcac	atgtgctctt tgtacagttt		853
taaaaagtgt aataaaatct gacatgtcaa araaaaaaa	mcy		896

<210> 243
 <211> 851
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..595

<220>
 <221> sig_peptide
 <222> 17..85
 <223> Von Heijne matrix
 score 3.70000004768372
 seq FLPLXRAFACRG/CQ

<220>
 <221> polyA_signal
 <222> 820..825

<220>
 <221> polyA_site
 <222> 840..851

<400> 243	
aagggggcgt ggggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc	52
Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu	
-20 -15	
ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg	100
Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro	
-10 -5 1 5	
gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga	148
Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg	
10 15 20	
ttc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat	196
Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp	
25 30 35	
aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa	244
Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu	
40 45 50	

tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa	292
Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu	
55 60 65	
tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa	340
Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu	
70 75 80 85	
aaa gaa gaa ttt att cac tca aga cta aaa act aaa ggc ctg ggc ctg	388
Lys Glu Glu Phe Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu	
90 95 100	
aga act gaa tca ggt cag aaa gca aca ttg aat gca gaa gaa atg gcg	436
Arg Thr Glu Ser Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala	
105 110 115	
gac ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cac atg tat	484
Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr	
120 125 130	
tat aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg	532
Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met	
135 140 145	
gga aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa	580
Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln	
150 155 160 165	
aag aag agg agc aac taggagtcga ctctgaccca gccagagtcg aggtttccac	635
Lys Lys Arg Ser Asn	
170	
aggaagcara tggagctcct ttcacagggg ctctgagaaa aactggagct gatctcaaga	695
agccccacat cttcctaagg ggccccatgg cctgtttggg ggcagggtag gtccctggggc	755
actgtggggc gcctgcctgc tgatgtgggc tctaggccag cttgtttgtca cgtacgtggt	815
gtgaaataaa gcccaagcac tgggaaaaaa aaaaaa	851

<210> 244
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 89..334

<220>
 <221> sig_peptide
 <222> 89..130
 <223> Von Heijne matrix
 score 3.59999990463257
 seq AFTLXSLQALL/CV

<220>
 <221> polyA_signal
 <222> 462..467

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 <221> polyA_site
 <222> 484..495

<400> 244	
agtaggaasg cgccgscgt ggaggcgcca cgtcccttgc sgcgggggga gagamatcgc	60
ttggacttcg gggcggcctc ggacggcc atg gcc ttt acc ctg tas tca ctg	112
Met Ala Phe Thr Leu Xaa Ser Leu	

-10

ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag	160
Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu	
-5 1 5 10	
gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt	208
Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly	
15 20 25	
gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att	256
Gly Phe Gly Glu Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile	
30 35 40	
cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca	304
Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser	
45 50 55	
att gca att gtg tta ctt tta tta ttt gga tgaatwtcat tggagaaaat	354
Ile Ala Ile Val Leu Leu Leu Leu Phe Gly	
60 65	
ggakactcag aaraggacat gccaktaraa kttattactt tggtcattat tggaatattt	414
atatcttagc tggctgacct tgcacttgtc aaaaatgtaa agctgaaaat aaaaccaggg	474
tttctattta aaaaaaaaaa a	495

<210> 245

<211> 884

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..614

<220>

<221> sig_peptide

<222> 21..83

<223> Von Heijne matrix

score 10

seq LWALAMVTRPASA/AP

<220>

<221> polyA_signal

<222> 849..854

<220>

<221> polyA_site

<222> 873..884

<220>

<221> misc_feature

<222> 574

<223> n=a, g, c or t

<400> 245

aataccttag accctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc	53
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala	
-20 -15	
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca	101
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro	
-10 -5 1 5	
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg	149

Glu	Leu	Ala	Gln	His	Glu	Glu	Leu	Thr	Leu	Leu	Phe	His	Gly	Thr	Leu		
			10					15					20				
cag	ctg	ggc	cag	gcc	ctc	aac	ggt	gtg	tac	agg	acc	acg	gag	gga	cgg	197	
Gln	Leu	Gly	Gln	Ala	Leu	Asn	Gly	Val	Tyr	Arg	Thr	Thr	Glu	Gly	Arg		
		25				30					35						
ctg	aca	aag	gcc	agg	aac	agc	ctg	ggt	ctc	tat	ggc	cgc	aca	ata	gaa	245	
Leu	Thr	Lys	Ala	Arg	Asn	Ser	Leu	Gly	Leu	Tyr	Gly	Arg	Thr	Ile	Glu		
	40				45						50						
ctc	ctg	ggg	cag	gag	gtc	agc	cgg	ggc	cgg	gat	gca	gcc	cag	gaa	ctt	293	
Leu	Leu	Gly	Gln	Glu	Val	Ser	Arg	Gly	Arg	Asp	Ala	Ala	Gln	Glu	Leu		
55				60					65					70			
cgg	gca	agc	ctg	ttg	gaa	act	car	atg	gag	gag	gat	att	ctg	cas	ctg	341	
Arg	Ala	Ser	Leu	Leu	Glu	Thr	Gln	Met	Glu	Glu	Asp	Ile	Leu	Xaa	Leu		
			75					80					85				
cag	gca	rag	gcc	aca	gct	gag	gtg	ctg	ggg	gag	gtg	gcc	cag	gca	car	389	
Gln	Ala	Xaa	Ala	Thr	Ala	Glu	Val	Leu	Gly	Glu	Val	Ala	Gln	Ala	Gln		
			90					95				100					
aag	gtg	cta	cgg	gac	agc	gtg	cag	cgg	cta	daa	ktc	cag	ctg	arg	asc	437	
Lys	Val	Leu	Arg	Asp	Ser	Val	Gln	Arg	Leu	Xaa	Xaa	Gln	Leu	Xaa	Xaa		
		105				110					115						
gcc	tgg	ctg	ggc	cct	gcc	tac	cga	aaa	ttt	gar	gtc	tta	aag	gcy	ccc	485	
Ala	Trp	Leu	Gly	Pro	Ala	Tyr	Arg	Lys	Phe	Glu	Val	Leu	Lys	Ala	Pro		
	120			125							130						
cck	gam	aar	car	aac	cac	atc	cta	tgg	gcc	ctc	aca	ggc	cac	gtg	cak	533	
Pro	Xaa	Lys	Gln	Asn	His	Ile	Leu	Trp	Ala	Leu	Thr	Gly	His	Val	Xaa		
	135			140					145					150			
cgg	car	arg	cgg	gar	atg	gtg	gca	cag	cag	cwt	ckg	ctg	cna	car	atc	581	
Arg	Gln	Xaa	Arg	Glu	Met	Val	Ala	Gln	Gln	Xaa	Xaa	Leu	Xaa	Gln	Ile		
			155					160					165				
cag	gar	aaa	ctc	cac	aca	gcg	gcg	ctc	cca	gcc	tgaatctgcc	tggaatggaac	634				
Gln	Glu	Lys	Leu	His	Thr	Ala	Ala	Leu	Pro	Ala							
			170					175									
tgaggaccaa	tcattgctgca	aggaacactt	ccacgccccg	tgaggcccct	gtgcagggag	694											
gagctgcctg	ttcactggga	tcagccaggg	cgccggggcc	cacttctgag	cacagagcar	754											
agacagacgc	aggcggggac	aaaggcagag	gatgtagccc	cattggggag	gggtggagga	814											
aggacatgta	ccctttcatr	mctacacacc	cctcattaaa	gcavagtcgt	ggcatctcaa	874											
aaaaaaaaaa						884											

<210> 246
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..573

<220>
 <221> sig_peptide
 <222> 94..258
 <223> Von Heijne matrix
 score 4.69999980926514
 seq IGILCSLLGTVLL/WV

<220>
 <221> polyA_signal
 <222> 862..867

<220>
 <221> polyA_site
 <222> 886..897

<400> 246

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aagggcggtt gcctagcacc cggaagagcc gtcaacttag cgagcgcaac aggctgccgc      60
tgaggagctg gagctggtgg ggactgggcc gca atg gac aag ctg aag aag gtg      114
                               Met Asp Lys Leu Lys Lys Val
                               -55                               -50

ctg agc ggg cag gac acg gag gac cgg agc ggc ctg tcc gag gtt gtt      162
Leu Ser Gly Gln Asp Thr Glu Asp Arg Ser Gly Leu Ser Glu Val Val
                               -45                               -40                               -35

gag gca tct tca tta agc tgg agt acc agg ata aaa ggc ttc att gcg      210
Glu Ala Ser Ser Leu Ser Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala
                               -30                               -25                               -20

tgt ttt gct ata gga att ctc tgc tca ctg ctg ggt act gtt ctg ctg      258
Cys Phe Ala Ile Gly Ile Leu Cys Ser Leu Leu Gly Thr Val Leu Leu
                               -15                               -10                               -5

tgg gtg ccc agg aag gga cta cac ctc ttc gca gtg ttt tat acc ttt      306
Trp Val Pro Arg Lys Gly Leu His Leu Phe Ala Val Phe Tyr Thr Phe
1                               5                               10                               15

ggt aat atc gca tca att ggg agt acc atc ttc ctc atg gga cca gtg      354
Gly Asn Ile Ala Ser Ile Gly Ser Thr Ile Phe Leu Met Gly Pro Val
                               20                               25                               30

aaa cag ctg aag cga atg ttt gag cct act cgt ttg att gca act atc      402
Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile
                               35                               40                               45

atg gtg ctg ttg tgt ttt gca ctt acc ctg tgt tct gcc ttt tgg tgg      450
Met Val Leu Leu Cys Phe Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp
                               50                               55                               60

cat aac aag gga ctt gca ctt atc ttc tgc att ttg cag tct ttg gca      498
His Asn Lys Gly Leu Ala Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala
65                               70                               75                               80

ttg acg tgg tac agc ctt tcc ttc ata cca ttt gca agg gat gct gtg      546
Leu Thr Trp Tyr Ser Leu Ser Phe Ile Pro Phe Ala Arg Asp Ala Val
                               85                               90                               95

aaa aad tgt ttt gcc gtg tgt ctt gca taattcatgg ccagttttat      593
Lys Xaa Cys Phe Ala Val Cys Leu Ala
                               100                               105

gaagcttttg aaggcactat ggacagaagc tgggtggacag ttttgtwact atcttcgaaa      653
cctctgtctt acagacatgt gccttttatc ttgcagcaat gtgttgcttg tgattcgaac      713
atttgagggt tactttttgga agcaacaata cattctcgaa cctgaatgtc agtagcacag      773
gatgagaagt gggttctgta tcttgtggag tggaatcttc ctcattgtacc tgtttcctct      833
ctggatgttg tcccactgaa ttcccatgaa tacaaaccta ttcagcaaca gcaaaaaaaaa      893
aaaa                                                                897

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<210> 247
 <211> 518
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..397

<220>

<221> sig_peptide
 <222> 74..127
 <223> Von Heijne matrix
 score 7.69999980926514
 seq LLLLPVLGLLVSS/KT

<220>
 <221> polyA_signal
 <222> 472..477

<220>
 <221> polyA_site
 <222> 507..518

<400> 247
 aaagaaagag ctgcsgtgca ggaattcgtg tgccggattt ggtagctga gccaccgag 60
 aggcgccctgc agg atg aaa gct ctc tgt ctc ctc ctc ctc cct gtc ctg 109
 Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu
 -15 -10
 ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc 157
 Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
 -5 1 5 10
 aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata 205
 Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
 15 20 25
 agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg 253
 Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
 30 35 40
 gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc 301
 Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
 45 50 55
 gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag 349
 Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
 60 65 70
 tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt cgt gtg cag ccc 397
 Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
 75 80 85 90
 tgaggtcgcg cgcagcgcg gcacagcgcg ggccggaggcg gctccaggtc cggagggggtt 457
 gcggggggagc tggaaataaa cctggagatg atgatgatga tgatgatgga aaaaaaaaaa 517
 a 518

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 <222> 51..242

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 <223> Von Heijne matrix
 score 6.5
 seq SCLCPALFPGTSS/FI

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                                     Met Ile
tcc agg cag ctg aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc      104
Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro
-20          -15          -10          -5
ggg act tcc tcc ttt att gta gca ctg agc tcc cca gcc gat ctg tac      152
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr
                1          5          10
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa      200
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys
        15          20          25
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta      242
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
        30          35          40
tgattttgct gaattttaaa taaaatgaaa accataaatt acatratgct tttattgach      302
cttgacmact ggcctaaata aaaaractct gactccaaaa aaaaaaaaa      350

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<222> 111..191

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<222> 111..155
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      seq FLXLMTLTTHVHS/SA

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<222> 965..970

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<222> 332
<223> n=a, g, c or t

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atccgataca gaacatgcag taatgtggac tgcccaccag aagcaggtga tttccgagct      60

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Met Gly	
-15	
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag	164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys	
-10 -5 1	
cca aat gaa caa ccc tgg ttg ttg aac tagcacctaa ggtcttarat	211
Pro Asn Glu Gln Pro Trp Leu Leu Asn	
5 10	
ggtacgcggt gctatacaga atctttggat atgtgcatca gtgggtttatg ccaaattggt	271
ggctgcgatc accagctggg aagcaccgtc aaggaarata actgtgggggt ctgcaacrga	331
natgggtcca cctgccggtt ggtccgaggg cartataaat ccakctctc cgcaaccaa	391
tcrgatgata ctgtgggtgc aattccctat ggaagtakac atattcgcct tgtcttaaaa	451
ggtcctgatc acttatatct ggaarccawa accctccagg ggactaawgg tgaaaacagt	511
ctcasctcca caggaacttt ccttgtggac aattctagt tggacttcca gaawtttcca	571
gacwdagaga tactgagaat ggctggacca ctcacagcag atttcattgt caawattcgt	631
aactcgggct ccgctgacag tacagtccag kkatcttct atcaaccat catccaccga	691
tggagggara cggatttctt tccttgctca gcaacctgtg gaggagggtta tcagctgaca	751
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taccagaga acatcaaacc caaacccaag cttcaggagt gcaacttgga tccttgtcca	871
gccaggtcag tcaaatttgc tagttcattt gtcataaaca taactcaagt tccaaatagg	931
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aaaaa	996

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 <222> 45..107
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 seq LLTIVGLILPTRG/QT

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Met Ser Pro Ser	
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Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg	
-15 -10 -5	
gga cag acg ttg aaa gat acc acg tcc agt tct tca gca gac tca act	152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr	

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      1           5           10           15
atc atg gac att cag gtc ccg aca cga gcc cca gat gca gtc tac aca      200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
      20           25           30
gaa ctc cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca      248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
      35           40           45
cca caa ccc cag acc cag acc cag caa ctg gaa gga acg gat ggg cct      296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
      50           55           60
cta gtg aca gat cca gag aca cac wak agc mcc aaa gca gct cat ccc      344
Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys Ala Ala His Pro
      65           70           75
act gat gac acc acg acg ctc tct gag aga cca tcc cca agc aca kac      392
Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Xaa
      80           85           90           95
gtc cat dac aga ccb cba kda ccc tca akc cat ctg gtt ttc atg agg      440
Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu Val Phe Met Arg
      100           105           110
atg acc cct tct tct atg atg aac aca ccc tcc gga aac sgg ggc tgt      488
Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly Asn Xaa Gly Cys
      115           120           125
tgg tcg cag ctg tgc tgt tca tca cag gca tca tca tcc tca cca gtg      536
Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser Ser Pro Val
      130           135           140
gca agt gca ggc agc tgt ccc ggt tat gcc gga atc att gca ggt gag      584
Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile Ile Ala Gly Glu
      145           150           155
tcc atc aga aac agg agc tgacaacctg ctgggcaccc gaagaccaag      632
Ser Ile Arg Asn Arg Ser
      160           165
ccccctgccca gctcaccgtg cccagcctcc tgcacccct cgaagagcct ggccagagag      692
ggaagacaca gatgatgaag ctggagccag ggctgccggt ccgagtcctcc tacctcccc      752
aaccctgccc gccctgaag gctacctggc gccttggggg ctgtccctca agttatctcc      812
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<211> 593

<212> DNA

<213> Homo sapiens

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<221> CDS

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<222> 24..101

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seq LLLLLCGPSQDQC/RP

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<222> 563..568

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<222> 583..593

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<221> misc_feature

<222> 3,485,517,556

<223> n=a, g, c or t

<400> 251

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                        Met Glu Thr Gly Ala Leu Arg Arg Pro Gln
                        -25                                -20

ctt ctc ccg ttg ctg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc      101
Leu Leu Pro Leu Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys
-15                                -10                                -5

cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc      149
Arg Pro Val Leu Gln Asn Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser
1                                5                                10                                15

ttg gaa gtg ccc act ggg aga gaa gga aag gaa ggt ggg gat cgg gga      197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly
20                                25                                30

cca ggg cta akt ggg gcc act cca gcc agg agc cct cag ggc aag gag      245
Pro Gly Leu Xaa Gly Ala Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu
35                                40                                45

atg ggg aga caa agg acc aga aag gtg aag ggc cct gct tgg akt cac      293
Met Gly Arg Gln Arg Thr Arg Lys Val Lys Gly Pro Ala Trp Xaa His
50                                55                                60

aca gca aat cag gaa cta aac agg atg agg tct ctg tct tct ggc tcc      341
Thr Ala Asn Gln Glu Leu Asn Arg Met Arg Ser Leu Ser Ser Gly Ser
65                                70                                75                                80

gtg cca gtg ggg cat ctg gag ggt ggc acg gtc aag ctt cag aag gac      389
Val Pro Val Gly His Leu Glu Gly Gly Thr Val Lys Leu Gln Lys Asp
85                                90                                95

acg ggc ctc cat tcc tgc ara gat ggt atg gct tct ctt gaa ggg acg      437
Thr Gly Leu His Ser Cys Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr
100                                105                                110

cca gct tca gtc ctg gct gat gct tgc cca gga ttc cat gat gtg aan      485
Pro Ala Ser Val Leu Ala Asp Ala Cys Pro Gly Phe His Asp Val Xaa
115                                120                                125

gtt car arg gcc cta ttt ggg tta agt ggg ana rta ctg tgg ctg aaa      533
Val Gln Xaa Ala Leu Phe Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys
130                                135                                140

acc cac ttc tgc ctt tct att ana ctt taaataaact ctgaaracct      580
Thr His Phe Cys Leu Ser Ile Xaa Leu
145                                150

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<211> 1114

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<213> Homo sapiens

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<222> 109..558

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 <222> 109..273
 <223> Von Heijne matrix
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 seq VAFMLTLPLVCK/VQ

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 <222> 1104..1114

<400> 252
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 Met Ala Thr
 -55
 aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga 165
 Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg
 -50 -45 -40
 ctt tgt gat aag gct gaa gct tgg ggc atc gtc cta gaa acg gtg gcc 213
 Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu Thr Val Ala
 -35 -30 -25
 aca gcc ggg gtt gtg acc tcg gtg gcc ttc atg ctg act ctc ccg atc 261
 Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile
 -20 -15 -10 -5
 ctc gtc tgc aag gtg cag gac tcc aac agg cga aaa atg ctg cct act 309
 Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met Leu Pro Thr
 1 5 10
 cag ttt ctc ttc ctc ctg ggt gtg ttg ggc atc ttt ggc ctc acc ttc 357
 Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly Leu Thr Phe
 15 20 25
 gcc ttc atc atc gga ctg gac ggg agc aca ggg ccc aca cgc ttc ttc 405
 Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr Arg Phe Phe
 30 35 40
 ctc ttt ggg atc ctc ttt tcc atc tgc ttc tcc tgc ctg ctg gct cat 453
 Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His
 45 50 55 60
 gct gtc agt ctg acc aag ctc gtc cgg ggg agg aaa gcc cct ttc cct 501
 Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala Pro Phe Pro
 65 70 75
 gtt ggt gat tct ggg tct ggc cgt ggg ctt cag cct agt cca gga tgt 549
 Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser Pro Gly Cys
 80 85 90
 tat cgc tat tgaatatatt gtcttgacca tgaataggac caacgtcaat 598
 Tyr Arg Tyr
 95
 gtctttttctg agcttttccgc tcctcgtcgc aatgaaaact ttgtcctcct gctcacctac 658
 ktctctttct tgaaggcgc gaccttctc wtgtcctcct tcaccttctg tggtkccttc 718
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 tgggtggcct ggatcaccct gctcatgctt cctgactttg accgcragggtg ggatgacacc 838
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 gagttttggc tgctcacaaa gcaackaaac cccatggatt atcctgttga ggatgctttc 958
 tgtaaaccctc aactcgtgaa gaagagctat ggtgtggrga acagagccta skctcaagag 1018
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<212> DNA
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 <222> 420
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 gagcaag atg ctg agc aag ggt ctg aag cgg aaa cgg gag gag gag gag 169
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
 -30 -25 -20
 gag aag gaa cct ctg gca gtc gac tcc tgg tgg cta gat cct ggc cac 217
 Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
 -15 -10 -5
 gca gcg gtg gca cag gca ccc ccg gcc gtg gcc tct agc tcc ctc ttt 265
 Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
 1 5 10 15
 gac ctc tca gtg ctc aag ctc cac cac agc ctg cag vrr agt rag ccg 313
 Asp Leu Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro
 20 25 30
 gac ctg cgg cac ctg gtg ctg gtc atr aac act ctg cgg cgc atc cag 361
 Asp Leu Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln
 35 40 45
 gcg tcc atg gca ccc gcg gct gcc ctg cca cct gtg cct acc cca cct 409
 Ala Ser Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro
 50 55 60
 gca gcc ccc ant gtg gct gac aac tta ctg gca agc tcg gac gct gcc 457
 Ala Ala Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala
 65 70 75
 ctt tca gcc tcc atg gcc arm ctc ctg gar gac ctc agc cac att gag 505
 Leu Ser Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu
 80 85 90 95
 ggc ctg agt cag gct ccc caa ccc ttg gca gac gag ggg cca cca ggc 553
 Gly Leu Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly
 100 105 110

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Arg	Ser	Ile	Gly	Gly	Xaa	Pro	Pro	Xaa	Leu	Gly	Ala	Leu	Asp	Leu	Leu		
			115					120					125				
ggc	cca	gcc	act	ggc	tgt	cta	ctg	gac	aat	ggg	ctt	gag	ggc	ctg	ttt		649
Gly	Pro	Ala	Thr	Gly	Cys	Leu	Leu	Asp	Asn	Gly	Leu	Glu	Gly	Leu	Phe		
		130					135				140						
gag	gat	att	gac	acc	tct	atg	tat	gac	aat	gaa	ctt	tgg	gca	cca	gcc		697
Glu	Asp	Ile	Asp	Thr	Ser	Met	Tyr	Asp	Asn	Glu	Leu	Trp	Ala	Pro	Ala		
	145					150				155							
tct	gag	ggc	ctc	aaa	cca	ggc	cct	gag	gat	ggg	ccg	ggc	aag	gag	gaa		745
Ser	Glu	Gly	Leu	Lys	Pro	Gly	Pro	Glu	Asp	Gly	Pro	Gly	Lys	Glu	Glu		
160					165				170					175			
gct	ccg	gag	ctg	gac	gag	gcc	gaa	ttg	gac	tac	ctc	atg	gat	gtg	ctg		793
Ala	Pro	Glu	Leu	Asp	Glu	Ala	Glu	Leu	Asp	Tyr	Leu	Met	Asp	Val	Leu		
			180						185					190			
gtg	ggc	aca	cag	gca	ctg	gag	cga	ccg	ccg	ggg	cca	ggg	cgc				835
Val	Gly	Thr	Gln	Ala	Leu	Glu	Arg	Pro	Pro	Gly	Pro	Gly	Arg				
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<222> 59..505

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<222> 59..358

<223> Von Heijne matrix

score 3.70000004768372

seq LASSFLFTMGGLG/FI

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<222> 1042..1047

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<221> polyA_site

<222> 1062..1073

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<222> 8..9

<223> n=a, g, c or t

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Met	Glu	Thr	Leu	Tyr	Arg	Val	Pro	Phe	Leu	Val	Leu	Glu	Cys	Pro	Asn	
-100					-95				-90						-85	
ctg	aag	ctg	aag	aag	ccg	ccc	tgg	ttg	cac	atg	ccg	tcg	gcc	atg	act	154
Leu	Lys	Leu	Lys	Lys	Pro	Pro	Trp	Leu	His	Met	Pro	Ser	Ala	Met	Thr	
				-80				-75						-70		
gtg	tat	gct	ctg	gtg	gtg	gtg	tct	tac	ttc	ctc	atc	acc	gga	gga	ata	202
Val	Tyr	Ala	Leu	Val	Val	Val	Ser	Tyr	Phe	Leu	Ile	Thr	Gly	Gly	Ile	
			-65					-60					-55			
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Ile	Tyr	Asp	Val	Ile	Val	Glu	Pro	Pro	Ser	Val	Gly	Ser	Met	Thr	Asp	
		-50					-45					-40				
gaa	cat	ggg	cat	cag	agg	cca	gta	gct	ttc	ttg	gcc	tac	aga	gta	aat	298
Glu	His	Gly	His	Gln	Arg	Pro	Val	Ala	Phe	Leu	Ala	Tyr	Arg	Val	Asn	
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Gly	Gln	Tyr	Ile	Met	Glu	Gly	Leu	Ala	Ser	Ser	Phe	Leu	Phe	Thr	Met	
	-20				-15				-10					-5		
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Gly	Gly	Leu	Gly	Phe	Ile	Ile	Leu	Asp	Gly	Ser	Asn	Ala	Pro	Asn	Ile	
			1				5					10				
cca	aaa	ctc	aat	aga	ttc	ctt	ctt	ctg	ttc	att	gga	ttc	gtc	tgt	gtc	442
Pro	Lys	Leu	Asn	Arg	Phe	Leu	Leu	Leu	Phe	Ile	Gly	Phe	Val	Cys	Val	
		15				20					25					
cta	twr	agt	ttt	tkc	ayg	gct	aga	gta	ttc	atg	aga	atg	aaa	ctg	ccg	490
Leu	Xaa	Ser	Phe	Xaa	Xaa	Ala	Arg	Val	Phe	Met	Arg	Met	Lys	Leu	Pro	
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ggc	tat	ctg	atg	ggg	tagagtgcct	ttgasaagaa	atcagtgat	actggatttg								545
Gly	Tyr	Leu	Met	Gly												
45																
ctcctgtcaa	wgaastttta	aaggctgtmc	caatcctcta	atatgaaatg	tggaagaa											605
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ctagaatttc	ttcttggtat	taaagagaca	agttttatcac	agaatttttt	ttcctgctgg											725
cctattgcta	taccaatgat	gttgagtggc	attttctttt	tagtttttca	ttaaaatata											785
ttccatatct	acaactataa	tatcaaataa	agtgattatt	ttttacaacc	ctcttaacat											845
tttttgga	tgacatttct	gatttttcaga	aattaacata	aaatccagaa	gcaagattcc											905
gtaagctgag	aactctggac	agttgatcag	ctttacctat	gggtgctttgc	ctttaactag											965
agtggtgat	ggtagattat	ttcagatatg	tatgtaaaac	tggttctctga	acaataagat											1025
gtatgaacgg	agcagaaata	aataactttt	ctaattaaaa	aaaaaaaa												1073

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<212> DNA

<213> Homo sapiens

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<222> 1..207

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<221> sig_peptide

<222> 1..147

<223> Von Heijne matrix

score 7.59999990463257

seq HLPFLLLLSCVGX/XP

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<222> 784..789

<220>

<221> polyA_site

<222> 807..818

<220>

<221> misc_feature

<222> 422

<223> n=a, g, c or t

<400> 255

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atg cct ttc cat ttt ccg ttc ctt ggg ttt gtg tgt ctg cat ctc cat      48
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
                                -45                                -40                                -35
ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg      96
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
                                -30                                -25                                -20
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg      144
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Cys Val Gly
                                -15                                -10                                -5
gkc www ccc tcc tgt ctg cct tct tcc tcc act tgt gtc agc ttg cat      192
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
      1              5              10              15
ttt ttt att cct gac tgagtcacca caccctcttc ccctgatcaa agggaatatk      247
Phe Phe Ile Pro Asp
                                20
artttttaat ttggatcgac tgaggtgccg ggagaaactg cagkcccagg tatccmvaca      307
gccaccagga tgggtccctcg ccccccaccc accgcctctk cccacacctt tccaacgtgt      367
tgcattgctgg gaactggggg gtgtggggga aggggctgcc ggcttctttc aggangctga      427
rgtttggar gaaaatcaac ctgggaracc accccggccg cggcgccctca gtggacaggt      487
gggargaaaa gaaaacttct taccttggar garggacatc ccgcttcctt atccttagct      547
tttttggtgc tcctccccac tgcccctttt aatttatattg gttgtttgcg gaaggagggg      607
ggaagggggg aagctgggccc gggaactgtc cgaggtgctg agctggggcg ggaccggaat      667
cctcccggta gggtagcagg gactgagttg ggccctggggc cgtgtccaag gtgccaatga      727
tgccggccga cagarcgggc cgcactgtct gtctgtccgt ctgtcccgga aagaactata      787
aagcgctgga agcgctgca aaaaaaaaaa a      818
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<210> 256

<211> 971

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..734

<220>

<221> sig_peptide

<222> 12..101

<223> Von Heijne matrix
score 4.80000019073486
seq ILFCVGAVGACTL/SV

<220>

<221> polyA_signal

<222> 914..919

<220>

<221> polyA_site

<222> 961..971

<400> 256

aatacacaga a atg ggg act gcg agc aga agc aac atc gct cgc cat ctg	50
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu	
-30 -25 -20	
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act	98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr	
-15 -10 -5	
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag	146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu	
1 5 10 15	
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag	194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu	
20 25 30	
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac	242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn	
35 40 45	
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg	290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg	
50 55 60	
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act	338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr	
65 70 75	
tca aat gac agt gca att tac atc tgt gga ata gca ttc ccc agt gtg	386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val	
80 85 90 95	
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta	434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val	
100 105 110	
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct	482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala	
115 120 125	
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc	530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe	
130 135 140	
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata	578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile	
145 150 155	
aaa gaa gac tca caa aag aag aag agt gct cgg cgt att ttt cag gaa	626
Lys Glu Asp Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu	
160 165 170 175	
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa	674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln	
180 185 190	
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac	722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn	
195 200 205	
tat gaa agg cca tagaaacggt ttaattttca atgaagtcac tgaaaatcca	774
Tyr Glu Arg Pro	
210	
actccaggag ctatggcagt gttaatgaac atatatcatc aggtcttaaa aaaaaataaa	834
ggtaaactga aaagacaact ggctacaaag aaggatgccaa raatgtaagg aaactataac	894
taataktcat taccaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa	954

tttgccaaaa aaaaaaw

971

<210> 257

<211> 640

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 378..518

<220>

<221> sig_peptide

<222> 378..467

<223> Von Heijne matrix

score 5.5

seq SLMTCTTLINASA/IS

<220>

<221> polyA_signal

<222> 607..612

<220>

<221> polyA_site

<222> 628..640

<400> 257

agcctgggta akgcccaaga tggctgtctt cgccttagta ctctgttgaa gttggcgggg 60

acggttcctg tcatcttctt gggcttattt ggtgtgctgt tgaagggggg agactagaga 120

aatggcaggg aacctcttat cgggggcagg taggcgcctg tgggactggg tgcctctggc 180

gtgcagaagc ttctctcttg gtgtgcctag attgatcggt ataaggctca ctctcccgcc 240

cccaaagtg gttgatcggt ggaacgagaa aagggccatg ttcggagtgt atgacaacat 300

cgggatcctg ggaaactttg aaaagcacc caaagaactg atcagggggc ccatatggct 360

tgcaggttgg aaaggga atg aat tgc aac gtt gta tcc gaa aga gga aaa 410

Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys

-30 -25 -20

tgg ttg gaa gta gaa tgt tgc ctg atg acc tgc aca acc tta ata aac 458

Trp Leu Glu Val Glu Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn

-15 -10 -5

gca tcc gct atc tct aca aac act tta acc gac atg gga agt ttc gat 506

Ala Ser Ala Ile Ser Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp

1 5 10

aga aga gaa agc tgagaacttc ggaaaaggct catctgtcac cctggaraag 558

Arg Arg Glu Ser

15

ggaaactgta cttttccctg tgaggaaacg gctttgtatt ttctctgtaa taaaatgggg 618

cttctttgga aaaaaaaaaa aa 640

<210> 258

<211> 745

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 110..304

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<220>
<221> sig_peptide
<222> 110..193
<223> Von Heijne matrix
      score 4.59999990463257
      seq PLQWSLLVAVVAG/SV

<220>
<221> polyA_signal
<222> 708..713

<220>
<221> polyA_site
<222> 732..743

<400> 258
acttccgcct gcgcctgcgc agcvcagctc cshgagccct gccaaacctg gtgaacttgg      60
gtctgtcccg ggtggacgac gccgtggctg ccaagcaccg gccaccggc atg gcc ttt      118
                                     Met Ala Phe
ggc ttg cag atg ttc att cag agg aag ttt cca tac cct ttg cag tgg      166
Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp
-25                               -20                               -15                               -10
agc ctc cta gtg gcc gtg gtt gca ggc tct gtg gtc agc tac ggg gtg      214
Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val
                               -5                               1                               5
acg aga gtg gag tcg gag aaa tgc aac aac ctc tgg ctc ttc ctg gag      262
Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu
                               10                               15                               20
acc gga cag ctc ccc aaa gac agg agc aca gat cag ara agc      304
Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa Ser
                               25                               30                               35
taggagagct ccagcagggg cacagargat tgggggcagg argartcttg aacacakcct      364
tcatgcccc tgaccccagg ccgaccctcc ccacacccta gggtagccca gtcgtatcct      424
ctgtccgcgt gtgtggccag gcctgacaaa cmcctgcaga tggctgctgc cccaacctgg      484
gacctgcca ggaggttgga gcagaaaggg ctctccctgg ggtggtgttt ctctctagg      544
gtattgggat gcatgttctg cactgccagc agagaggggtg tgtctggggg ccaccaccta      604
tgggacacgg ggtcgaaggg gcctgtacac tctgtcattt cctttctagc ccctgcatct      664
ccaacaagtc caaggtgaca gctggtgcta ggggcgtggg gttaataaat ggcttatcct      724
tctctccaaa araaaaaaam c      745

<210> 259
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 201..419

<220>
<221> sig_peptide
<222> 201..272
<223> Von Heijne matrix
      score 6.40000009536743
      seq LSYLPLWLGPWP/CS

<220>

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<221> polyA_signal

<222> 601..606

<220>

<221> polyA_site

<222> 627..637

<400> 259

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acaaaatata attgcctcts ccctctccca tttctctctt tgggagcaat ggtcacagtc      60
cctggtacct gaaaaggtag ctaggtctag gcccttcttc cctttccctt cctctccctt      120
accccagaac tttggctccc tttcccttct ctctctggta gctccaggag gcctgtgatc      180
cagctccctg cctagcatcc atg acc tgt tgg atg tta cct cca atc agt ttc      233
                Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe
                        -20                                -15

ctg tcc tac ctg cct ctt tgg ctt gga cct ata tgg cca tgc tct ggc      281
Leu Ser Tyr Leu Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly
                -10                                -5                                1

tct acc ctt ggg aag cct gat ccc ggt gtg tgg ccc agc ttg ttc agg      329
Ser Thr Leu Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg
        5                                10                                15

ccc tgg gat gct gca tct cca ggc aac tat gca ctt tcc cgg gga rar      377
Pro Trp Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa
20                                25                                30                                35

aac cak tat gav aak tgg ggg cag ggc aca cat tca tct ttg      419
Asn Xaa Tyr Xaa Xaa Trp Gly Gln Gly Thr His Ser Ser Leu
        40                                45

targaaggtc tggcctgggg tcrngtgaag gagggccag gtcagttctg ggggtccagt      479
gacctgcttt gccattctcc tgggtgccgt gctgctccct gtttctggag ctggatgttc      539
cccacctggc agttgagctg cctgagccaa tgtgtctgtc tttggtaact gagtgaacca      599
taataaaggg gaacatttgg ccctgtgaaa aaaaaaaaaa      637
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<210> 260

<211> 1315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 123..302

<220>

<221> sig_peptide

<222> 123..176

<223> Von Heijne matrix
score 4.30000019073486
seq WTCLKSFPSPTSS/HA

<220>

<221> polyA_signal

<222> 1279..1284

<220>

<221> polyA_site

<222> 1301..1312

<400> 260

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aagagcatcc tgcgccccgg cgcggggccc tgcggtagcc tcaggccctt ccctggacc      60
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cgccgcagag ccagtgcaga atacagaaac tgcagccatg accacgcacg tcacctgga 120
ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg 167
Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro
-15 -10 -5
acc agc agc cat gca tgc agc ctc cac ctt cct cca tca tgt acc agg 215
Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg
1 5 10
cta act ttg aca caa act ttg agg aca gga atg cat ttg tca cgg gca 263
Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala
15 20 25
ttg caa ggt aca ttg acc agg cta cag tcc act cca gca tgaatgarat 312
Leu Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
30 35 40
gctggaggaa ggacatgakt atgcggtcat gctgtacacc tggcgcagct gttccccgggc 372
cattccccag gtgaaatgca acragcagcc caaccgakta raratctatg araaracagt 432
araggtgctg gagccggagg tcaccaagct catgaagtcc atgtattttc arcgcaaggc 492
catcgagcgg ttctgcascg aggtgaagcg gctgtgccat gccgagcgca ggaaggactt 552
tgtctctgag gcctacctcc tgacccttgg caagttcatc aacatgtttg ctgtcctgga 612
tgagctaaag aacatgaast gcagcgtcaa raatgaccac tctgcctaca agagggcagc 672
acagttcctg cggaagatgg cagatcccca gtctatccag gagtcgcaga acctttccat 732
gttctctggc aaccacaaca ggatcaccca gtgtctccac cagcaacttg aagtgatccc 792
aggctatgag gagctgctgg ctgacattgt caacatctgt gtggattact acgagaacaa 852
gatgtacctg actcccagtg agaaacatat gtcctcctcaag gtaaaaactcc cctgaggccg 912
caccatgga gcctgggctt accctctcac cttcttctta ttaaaaatcc gttttaaaaa 972
acaatgtttc ttttttctta aacattgata cagatcttac ggcacataat ggtttgtaac 1032
ctgttccttt cctgtaatat aatataccgt agtcaccttt ccagatgtca ttaaggctat 1092
ttctacaatg ttatgtgtaa tgactgccaa gtattctgtt gtattggaac attgtcatgt 1152
aacatatccc ctgtggttgg atatttgcta aacttcattg aacacccttg tagcagtttt 1212
tgtgcacatc tttttgtcaa ggcaaacttc ctagaagaga aattgctggc tcaaagggaa 1272
aaacagaata aatcgttttt tttatttcaa aaaaaaaaaa ccc 1315

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<210> 261
<211> 1035
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..673

<220>
<221> sig_peptide
<222> 98..376
<223> Von Heijne matrix
score 5.59999990463257
seq VLLLRQLFAQAEK/WY

<220>
<221> polyA_site
<222> 1025..1035

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<400> 261
aattttcygt ggtccaacta ccctcggcga tcccaggctt ggccggggcac cgcttggcct 60
ctcccgttcc tttaggctgc cgccgctgcc tgccgcc atg gca gag ttg ggc cta 115
Met Ala Glu Leu Gly Leu
-90
aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt 163

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Asn	Glu	His	His	Gln	Asn	Glu	Val	Ile	Asn	Tyr	Met	Arg	Phe	Ala	Arg		
		-85					-80					-75					
tca	aag	aga	ggc	ttg	aga	ctc	aaa	act	gta	gat	tcc	tgc	ttc	caa	gac	211	
Ser	Lys	Arg	Gly	Leu	Arg	Leu	Lys	Thr	Val	Asp	Ser	Cys	Phe	Gln	Asp		
		-70					-65				-60						
ctc	aag	gag	agc	agg	ctg	gtg	gag	gac	acc	ttc	acc	ata	gat	gaa	gtc	259	
Leu	Lys	Glu	Ser	Arg	Leu	Val	Glu	Asp	Thr	Phe	Thr	Ile	Asp	Glu	Val		
		-55				-50				-45					-40		
tct	gaa	gtc	ctc	aat	gga	tta	caa	gct	gtg	gtt	cat	agt	gag	gtg	gaa	307	
Ser	Glu	Val	Leu	Asn	Gly	Leu	Gln	Ala	Val	Val	His	Ser	Glu	Val	Glu		
				-35					-30					-25			
tct	gag	ctc	atc	aac	act	gcc	tat	acc	aat	gtg	tta	ctt	ctg	cga	cag	355	
Ser	Glu	Leu	Ile	Asn	Thr	Ala	Tyr	Thr	Asn	Val	Leu	Leu	Leu	Arg	Gln		
			-20					-15					-10				
ctg	ttt	gca	caa	gct	gag	aag	tgg	tat	ctt	aag	cta	cag	aca	gac	atc	403	
Leu	Phe	Ala	Gln	Ala	Glu	Lys	Trp	Tyr	Leu	Lys	Leu	Gln	Thr	Asp	Ile		
		-5					1			5							
tct	gaa	ctt	gaa	aac	cga	gaa	tta	tta	gaa	caa	ktt	gca	gaa	ttt	gaa	451	
Ser	Glu	Leu	Glu	Asn	Arg	Glu	Leu	Leu	Glu	Gln	Xaa	Ala	Glu	Phe	Glu		
		10				15				20				25			
aaa	gca	rav	att	aca	tct	tca	aac	aaa	aag	ccc	atc	tta	dat	gtc	aca	499	
Lys	Ala	Xaa	Ile	Thr	Ser	Ser	Asn	Lys	Lys	Pro	Ile	Leu	Xaa	Val	Thr		
			30						35					40			
aas	cca	aaa	ctt	gct	cca	ctt	aat	gaa	ggt	gga	aca	gca	aaa	ctc	cta	547	
Xaa	Pro	Lys	Leu	Ala	Pro	Leu	Asn	Glu	Gly	Gly	Thr	Ala	Lys	Leu	Leu		
			45					50					55				
aac	aag	gta	ata	tgt	att	att	ttg	aga	aac	gga	aag	tct	ctc	att	ctg	595	
Asn	Lys	Val	Ile	Cys	Ile	Ile	Leu	Arg	Asn	Gly	Lys	Ser	Leu	Ile	Leu		
		60					65					70					
tcc	tgt	cat	tgc	cta	ggg	tgg	aga	aac	aaa	agt	gga	agg	ttt	gtt	tca	643	
Ser	Cys	His	Cys	Leu	Gly	Trp	Arg	Asn	Lys	Ser	Gly	Arg	Phe	Val	Ser		
		75				80					85						
ggt	cct	ctg	agg	ata	att	agt	cca	ttg	cag	tagttttact	tgatgggtacc					693	
Gly	Pro	Leu	Arg	Ile	Ile	Ser	Pro	Leu	Gln								
		90				95											
ccatggggcca	gaagaggggca	tacttaacct	tctagagagc	ctgaagtagc	tcttgatcac											753	
acctttttcaa	ggtaaagtga	agagcatgaa	atthttggaca	gcgtttattg	atggacattt											813	
aaagttttgtg	atctgcggta	acaaggagaa	gggttttttaa	gtttataaaa	attattttatc											873	
aattagccgg	gtgtggtggt	acgtgcctat	agtcagagct	actcgggagg	ctgaggcagg											933	
agaattgctt	gaaccgga	ggtggaggtt	gcagtgcctt	gagatcacgc	cactgcactc											993	
tagcctgggc	gacagagcga	gactccatct	caaaaaaaaa	aa												1035	

<210> 262

<211> 696

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 17..463

<220>

<221> sig_peptide

<222> 17..232

<223> Von Heijne matrix

score 3.79999995231628

seq LMGLALAVYKCQS/MG

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<220>
<221> polyA_signal
<222> 657..662

<220>
<221> polyA_site
<222> 684..696

<400> 262
actcaaacag attccc atg aat ctc ttc atc atg tac atg gca ggc aat act      52
                Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr
                -70                                -65

atc tcc atc ttc cct act atg atg gtg tgt atg atg gcc tgg cga ccc      100
Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro
-60                -55                -50                -45

att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt      148
Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser
                -40                -35                -30

tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg      196
Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu
                -25                -20                -15

atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta      244
Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu
                -10                -5                1

cct aca cat gca tgc gat tgg tta gcc ttc att gag ccc cct gag aga      292
Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
5                10                15                20

atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg      340
Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
                25                30                35

cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca      388
Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
                40                45                50

gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac      436
Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn
                55                60                65

caa aaa act ctt ttc tcc atg gtg ggg tgacaggtcc taaaaggaca      483
Gln Lys Thr Leu Phe Ser Met Val Gly
                70                75

atgtgcatat tacgacaaac acaaaaaaac tataccataa cccagggctg aaaataatgt      543
aaaaaacttt atttttgttt ccagtacaga gcaaaacaac aacaaaaaaa cataactatg      603
taaacaaaaa aataactgct gctaaatcaa aaactgttgc agcatctcct ttcaataaat      663
taaatggttg araacaatgc aaaaaaaaaa aaa                                696

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<210> 263
<211> 868
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 263..481

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<220>
<221> sig_peptide
<222> 263..322

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<223> Von Heijne matrix
 score 11.1999998092651
 seq ILVVLMLGLPLAQA/LD

<220>

<221> polyA_site

<222> 858..868

<220>

<221> misc_feature

<222> 473

<223> n=a, g, c or t

<400> 263

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aagacacgcc tacgattaga ctcaggcagg cacctaccgg cgagcggccg crvgtgactc      60
ccaggcgagg cggtacctca cggtggtgaa gggtcacaggg ttgcagcact ccagtagac      120
caggagctcc gggaggcagg gccggcccca cgtcctctgc gcaccaccct gagttggatc      180
ctctgtgcgc caccctgag ttggatccag ggctagctgc tgttgacctc cccactccca      240
cgctgccctc ctgcctgcag cc atg acg ccc ctg ctc acc ctg atc ctg gtg      292
                        Met Thr Pro Leu Leu Thr Leu Ile Leu Val
                        -20                               -15
gtc ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt      340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10                               -5                               1                               5
gcc tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg      388
Ala Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met
                        10                               15                               20
gtt gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg      436
Val Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met
                        25                               30                               35
aag gtc agt aag tcc tgc gtg ccc cgc tgc ttc gar nac tgt gta      481
Lys Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Xaa Cys Val
                        40                               45                               50
tgatgggtac tccaagcacg cgtccaccac ctctgtctgc cagtacgacc tctgcaacgg      541
caccggcctt gccaccccg gacccctggc cctggccccc atcctcctgg ccaccctctg      601
gggtctcttc taaagcccc gaggcagacc cactcaagaa caaagctctc gagacacact      661
gctayaccct ckcacccakc tcaccctgcc tcaccctcca cactccctgc gacctcctca      721
gccatgcccc gggtcaggac tgtgggcaag aagacaccgg acctccccca accaccacac      781
gacctactt cgaggccttg acctttcgat gctgtgtggg atcccaaaag tgtccggctt      841
tgatgggctg atcagcaaaa aaaaaaa      868

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<210> 264

<211> 775

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 42..299

<220>

<221> sig_peptide

<222> 42..101

<223> Von Heijne matrix
 score 5.40000009536743
 seq WFWHSSALGLVLA/PP

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<220>
<221> polyA_site
<222> 762..775

<400> 264
aacgatacaa atggtaggcc ttcattgtgag ccagtdacta c atg aat ctt cat ttc      56
                                   Met Asn Leu His Phe
                                   -20
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca      104
Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro
-15              -10              -5              1
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt      152
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys
              5              10              15
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc      200
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr
              20              25              30
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa      248
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys
              35              40              45
aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cgg      296
Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg
50              55              60              65
cag tgaaactwkk ttcwcttcta aagcccttca tttcccacaa ggттаagctc      349
Gln
tcgaaacccc atttgatcct tggttcctat ttcgatcctc ctttggaatc tgaaaatcgg      409
tctccatgtt gtatgcaaat taaaakttgc cttgtttgtt actcttccaa cacaggggat      469
cagggaraaa gaggccttat ctgttcctcc atccccctg ttttgacaga ctgctaagaa      529
ttcctcagga cttccttttg ttggggattt tactttccca aaagtctgat ctgatttctt      589
tcaggggtag acaagcttgt cctagtgtc tgcttcaggt cttatcagaa gaaaccagg      649
aatagaaaag gtagatgcct tgacttttgt ccctgttgtg gggactaaag tgttttttgc      709
cagaattgtc aaaagctccg gttcaaactc tgtagagttt catggaaaaa caaaacaaaa      769
aaaaaa      775

<210> 265
<211> 1075
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 198..431

<220>
<221> sig_peptide
<222> 198..260
<223> Von Heijne matrix
      score 6.90000009536743
      seq LLACGSLLPGLWQ/HL

<220>
<221> polyA_site
<222> 1064..1074

<400> 265
atatatttct gaggcagtac ccattctcact tgtaaactta aaagacaccg cagagatttg      60
agggactcag aagtcaaata gagtaggtta aaaacctctt atttttcaaa ttaattgttt      120

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taagaaacaa gcatacctgt gtaagtgaag tatcttaatt tgtgttgaat caagttagga 180
gacagagatt ctcatga atg tgt cct gtg ttc tca aag cag ctg cta gcc 230
          Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala
          -20                               -15
tgt ggg tct ctc cta cct ggg tta tgg cag cac ctc aca gcc aat cac 278
Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His
-10                               -5                               1                               5
tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca 326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
          10                               15                               20
gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt 374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg
          25                               30                               35
tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac 422
Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr
          40                               45                               50
tct atc acc tagccattgt akccatacca agccgggctt cctacttccc 471
Ser Ile Thr
55
tctgctcccc ttggtttcct cctgtraart aaatctcact gacccttgat gcasctccaa 531
gcatatataa tatatatata ataaaaccat abtctaaaaa attcaaacca ggawaaataa 591
asccaraaat ttgtatggga aaaatctgca caaatatttatt tggccagcat gggtatcatg 651
gctctattga atttatcctt gaccgtcttt aaagccaaag caaacgggat aaagtgatca 711
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aaaacaattc ttakctgggc gcggtggctc wcacctgtar tcccaacact ttgggaggcc 831
saggtgggcg gatcatgagg tcgggagatc aamaccatcc tggctaacat ggtgaaaccc 891
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ctactcggga ggctgaggca agagaatggg gtgaacccca gggggcggag cctgcagtga 1011
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aaah 1075

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<210> 266
<211> 981
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 279..473

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<220>
<221> sig_peptide
<222> 279..362
<223> Von Heijne matrix
      score 4.40000009536743
      seq SCFLVALIIWCYL/RE

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<220>
<221> polyA_signal
<222> 944..949

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<220>
<221> polyA_site
<222> 970..981

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<400> 266
agaatcgtgt cttgtgtgcc ccggcggccg ggtgagctcc tcaaggtctc ggagggccga 60

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gggcagacac cggcgggagg gaggagcgtt actgctctct ctcttccagg gccgtccggg 120
cgctgagggt cataggctgg gcttcccgaa gccttcatcc gttgcccggg tcccgggagc 180
gggcccaccc tgccgccgag gaagaggacg accctgaccg cccattgag ttttctcca 240
gcaaagccaa ccctcaccgc tggtcgggtg gccatacc atg gga aag gga cat cag 296

```

Met Gly Lys Gly His Gln

-25

```

cgg ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg 344
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu

```

-20

-15

-10

```

atc atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg 392
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu

```

-5

1

5

10

```

aga cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag 440
Arg Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu

```

15

20

25

```

cct gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgctgggg 493
Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr

```

30

35

```

ctggcaggaa gggagccgac asccgccctt cggatttgat ktcacgtttg cccgtgactg 553
tcctggctat gcktgcgctc tcagcactra argacttggc tggaggatgg ggcacttggc 613
tatgctgatt cgcgtgaagg cggavcaaaa tctcagcaaa tcggaaactg ctctcscct 673
ggctcttgat ktccaaggat tccatcggca aaacttctca ratccttggg gaaggtttca 733
gttgactgt atgctgttgg atttgccaag tctttgtata acataatcat gtttccaaag 793
cacttctggg gacacttgct atccagtgtt agtttgcagg taatttgctt tctgagatag 853
aatatctggc agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc 913
acatgtgagt tttacacaac aacaaatgaa aataaatttt aattttataa tatgggaaaa 973
aaaaaaaa 981

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<210> 267

<211> 1031

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..644

<220>

<221> sig_peptide

<222> 12..92

<223> Von Heijne matrix

score 4

seq LTFSGVYGCIG/AT

<220>

<221> polyA_signal

<222> 1002..1007

<220>

<221> polyA_site

<222> 1020..1031

<400> 267

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acaccaagga g atg ctc ctt ctt agt att aca act gct tat aca ggt ctg 50
Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu

```

-25

-20

-15

```

gaa tta act ttc ttc tct ggt gta tat gga acc tgt att ggt gct aca 98

```


Glu	Leu	Thr	Phe	Phe	Ser	Gly	Val	Tyr	Gly	Thr	Cys	Ile	Gly	Ala	Thr		
				-10					-5					1			
aat	aaa	ttt	gga	gca	gaa	gag	ara	agc	ctt	att	gga	ctt	tct	ggc	att	146	
Asn	Lys	Phe	Gly	Ala	Glu	Glu	Xaa	Ser	Leu	Ile	Gly	Leu	Ser	Gly	Ile		
		5					10					15					
ttc	atc	ggc	att	gga	gaa	att	tta	ggt	gga	agc	ctc	ttc	ggc	ctg	ctg	194	
Phe	Ile	Gly	Ile	Gly	Glu	Ile	Leu	Gly	Gly	Ser	Leu	Phe	Gly	Leu	Leu		
	20					25					30						
agc	aag	aac	aat	cgt	ttt	ggt	aga	aat	cca	ggt	gtg	ctg	ttg	ggc	atc	242	
Ser	Lys	Asn	Asn	Arg	Phe	Gly	Arg	Asn	Pro	Val	Val	Leu	Leu	Gly	Ile		
	35			40					45					50			
ctg	gtg	cac	ttc	ata	gct	ttt	tat	cta	ata	ttt	ctc	aac	atg	cct	gga	290	
Leu	Val	His	Phe	Ile	Ala	Phe	Tyr	Leu	Ile	Phe	Leu	Asn	Met	Pro	Gly		
			55					60					65				
gat	gcc	ccg	att	gct	cct	ggt	aaa	gga	act	gac	agc	agt	gct	tac	atc	338	
Asp	Ala	Pro	Ile	Ala	Pro	Val	Lys	Gly	Thr	Asp	Ser	Ser	Ala	Tyr	Ile		
		70					75						80				
aaa	tcc	agc	aaa	raa	ttt	gcc	att	ctc	tgc	akt	ttt	ctg	tkg	ggc	ctt	386	
Lys	Ser	Ser	Lys	Xaa	Phe	Ala	Ile	Leu	Cys	Xaa	Phe	Leu	Xaa	Gly	Leu		
	85				90						95						
gga	aac	agc	tgc	ttt	aat	acc	cas	ctg	ctt	akt	atc	tkg	ggc	ttt	ctg	434	
Gly	Asn	Ser	Cys	Phe	Asn	Thr	Xaa	Leu	Leu	Xaa	Ile	Xaa	Gly	Phe	Leu		
	100				105					110							
tat	tct	gaa	rac	agc	gcc	cca	kca	ttt	gcc	atc	ttc	aat	ttt	ggt	cag	482	
Tyr	Ser	Glu	Xaa	Ser	Ala	Pro	Xaa	Phe	Ala	Ile	Phe	Asn	Phe	Val	Gln		
	115				120				125					130			
tct	att	tgc	gca	gcc	gtg	gca	ttt	ttc	tac	agc	aac	tac	ctt	ctc	ctt	530	
Ser	Ile	Cys	Ala	Ala	Val	Ala	Phe	Phe	Tyr	Ser	Asn	Tyr	Leu	Leu	Leu		
			135				140						145				
cac	tgg	caa	ctc	ctg	gtc	atg	gtk	atw	ttt	ggg	ttt	ttk	gga	aca	att	578	
His	Trp	Gln	Leu	Leu	Val	Met	Val	Ile	Phe	Gly	Phe	Xaa	Gly	Thr	Ile		
		150				155						160					
tct	ttc	ttc	act	gtg	gaa	tgg	gaa	sct	gcc	gcc	ttt	gta	scc	cgc	ggc	626	
Ser	Phe	Phe	Thr	Val	Glu	Trp	Glu	Xaa	Ala	Ala	Phe	Val	Xaa	Arg	Gly		
	165				170						175						
tct	gac	tac	cga	agt	atc	tgatctggtg	tccgtgaggg	gacacgtatg								674	
Ser	Asp	Tyr	Arg	Ser	Ile												
	180																
acctcagaaa	cacagctgga	cacagagctt	ggtggaagaa	gtcgcctttg	atcttcaacta											734	
tatattgggt	gatgttcagt	atggaaaatc	aagggtatata	gactgttata	tcagccagag											794	
tkgggtgttca	agtttacaga	tatgagttat	ttaaagcaag	tagaataagg	gaaagctggt											854	
ctgtcaactg	taattgttca	aagatgttgt	ttttcatttc	atctatctca	attcttataa											914	
tcatgttata	gaatgtaaat	gttttcttct	ctctcctgct	cttggttgaa	gatcctgcct											974	
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<210> 268

<211> 1283

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 91..459

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<221> sig_peptide

<222> 91..330

<223> Von Heijne matrix
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 seq LVLFLSLALLVTP/TS

<220>

<221> polyA_site

<222> 1271..1281

<400> 268

tattccttgg agttccacga ctgaattaag actgttgtgg grdcataat tttcaaatac	60
ttgccctata ttctgtgtga ggggttcacac atg agc aca tgg tat ttg gca ctt	114
Met Ser Thr Trp Tyr Leu Ala Leu	
-80 -75	
aat aag tcc tat aag aat aaa gac agc gtt agg att tat ctc agc ttg	162
Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu	
-70 -65 -60	
tgc aca gtg agc att aaa ttt aca tac ttt cat gat ata cag act aat	210
Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn	
-55 -50 -45	
tgt ctt aca aca tgg aaa cat tcg aga tgc aga ttt tat tgg gca ttt	258
Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe	
-40 -35 -30 -25	
ggg ggt tcc att tta cag cac tca gtg gat ccc ctt gtt ttg ttc cta	306
Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Leu Phe Leu	
-20 -15 -10	
agc ctg gcc ctg tta gtg aca ccc act tcc acc cct tct gct aar ata	354
Ser Leu Ala Leu Leu Val Thr Pro Thr Ser Thr Pro Ser Ala Lys Ile	
-5 1 5	
car agc ctt caa att gac ctc cct gga ggc tgg agg ctg gcc act gac	402
Gln Ser Leu Gln Ile Asp Leu Pro Gly Gly Trp Arg Leu Ala Thr Asp	
10 15 20	
agg atc ttt acc ctc tcc ccc gta ccc atg gac rgc ccc ctc atc ctt	450
Arg Ile Phe Thr Leu Ser Pro Val Pro Met Asp Xaa Pro Leu Ile Leu	
25 30 35 40	
cat cag ttg taaaggtaga tatttgttcc ttggagtcca acatcatgct	499
His Gln Leu	
gttcagaata taatgagatc aatagttgaa aaactagata tacatgccac ccwgacaaag	559
ctattaagtt attaagtgtc agccctggat cttggccttat tgtgaaatgt taattatttt	619
atcactcyat taagaagctg tgggctccat ctcagcattg aaaagggact aatttgctct	679
gttttggaaat tgaattagct ttcaggccas cagggcactg tttggtaaat tgctttttcc	739
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actggggagg ctgaggcarg araatcgctt gaacctggga ggcggagggt gcastragct	1219
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<210> 269

<211> 1777

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
 <222> 70..327

<220>
 <221> sig_peptide
 <222> 70..147
 <223> Von Heijne matrix
 score 9.60000038146973
 seq WLIALASWSWALC/RI

<220>
 <221> polyA_signal
 <222> 1741..1746

<220>
 <221> polyA_site
 <222> 1763..1774

<220>
 <221> misc_feature
 <222> 937
 <223> n=a, g, c or t

<400> 269
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 agagctaca atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg 111
 Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp
 -25 -20 -15
 cta ata gcc ttg gct tca tgg tct tgg gct ctg tgc cgt att tct ctt 159
 Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu
 -10 -5 1
 tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt 207
 Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu
 5 10 15 20
 ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat 255
 Leu Leu Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp
 25 30 35
 gta ttg ctt tat ttt ccw kaa cag yya tcc tct tca cgt ctt tat gat 303
 Val Leu Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp
 40 45 50
 tcc cat gcc cac tgg cmt tgc rca taaaaaatt ttcacagaa ccaaagatgg 357
 Ser His Ala His Trp Xaa Ser Xaa
 55 60
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 tataatttat tttcatggga atgcaggcaa cataggtcac aggttggcca aatgcattac 477
 ttatgttggg taacctcaaa gttaaccttt tgctgggtga ttatcgagga tatggaaaaa 537
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 tgatgactag acctgacctt gataaaaaca aaatttttct ttttggccgt tccttgggtg 657
 garcagtggc tattcatttg gcttctgaaa attcacatag gatttcagcc attatggtgg 717
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 ttatataatg tttccctttt tgattattgc attgtatttt aatttgtgca gaatgataaa 1137
 gaatgttcct tttagaagtg tgttatgtct gtacctgtct gaagagtgc attaaacttt 1197

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gaaaggactt cactgctcct ttacgatatt ccaaataggt ttttacattg gaaaaactaa 1257
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gggttatatc tatttttatg taaactctat ttttgttttt ggcaagaagt gaaattgaga 1677
cttatgtgca ggttgccatt gaattttgct ctggatgaat ctgagatcca gctttttctt 1737
acaaataaat gggaccctgt tttccaaaaa aaaaaamcm 1777

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<210> 270
<211> 970
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 12..497

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<220>
<221> sig_peptide
<222> 12..104
<223> Von Heijne matrix
      score 5.5
      seq LVGVLFVSVTTG/PW

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<220>
<221> polyA_signal
<222> 935..940

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<220>
<221> polyA_site
<222> 955..967

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<400> 270
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          Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
          -30                      -25                      -20
gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act 98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
          -15                      -10                      -5
aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg 146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
          1                      5                      10
ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca 194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
          15                      20                      25                      30
aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca 242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
          35                      40                      45
gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc 290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser
          50                      55                      60
agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag 338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
          65                      70                      75

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ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tgc      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser
   80                85                90
cat gtc tct ttt tct tgg atg gtt ggg agc aga tgc att tta cct tgg      434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
   95                100                105                110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg      482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp
                115                120                125
aat tgg gag cct aat tgatttcaty cttatttcaa tgcagattgt tggaccttca      537
Asn Trp Glu Pro Asn
                130
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact      597
aatgaaacat ttagaaaaac gcaattatat ccataaatat tttttaaaag aaacagattt      657
gagcctcctt gattttaata gagaacttct agtgtatgga tttaaagatt tctctttttc      717
attcatatac cattttatga gttctgtata attttttggtg gtttttggtt tggtgagtta      777
aagtatatta ttgtgagatt tatttaatag gacttccttt gaaagctgta taatagtgtt      837
tctcgggctt ctgtctctat gagagatagc ttattactct gatactcttt aatcttttac      897
aaaggcaagt tgccacttgt catttttggt tctgaaaaat aaaagtataa cttattcaca      957
aaaaaaaaaa mms                                                    970

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<212> DNA
<213> Homo sapiens

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<222> 90..383

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      score 4.90000009536743
      seq MLIMLGIFNVHS/AV

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<220>
<221> polyA_site
<222> 632..643

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atctctgccc ccctgcgagg gcatcctggg ctttctccca ccgcttttcg agcccgttg      60
cacctcggcg atccccgact cccttcttt atg gcg tgc ctc ctg tgc tgt ggg      113
                               Met Ala Ser Leu Leu Cys Cys Gly
                               -35                -30
ccg aag ctg gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc      161
Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile
                -25                -20                -15
atg ttg ata atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg      209
Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
                -10                -5                1
att gag gac gtt ccc ttc acg gag aaa gat ttt gag aac ggc ccc car      257

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Ile	Glu	Asp	Val	Pro	Phe	Thr	Glu	Lys	Asp	Phe	Glu	Asn	Gly	Pro	Gln	
5						10					15					
aac	ata	tac	aac	ctt	tac	rag	caa	ktc	agc	tac	aac	tgt	ttc	atc	gct	305
Asn	Ile	Tyr	Asn	Leu	Tyr	Xaa	Gln	Xaa	Ser	Tyr	Asn	Cys	Phe	Ile	Ala	
20				25					30				35			
gca	ggc	ctt	tac	ctc	ctc	gga	ggc	ttc	tct	ttc	tgc	caa	ktc	cgg		353
Ala	Gly	Leu	Tyr	Leu	Leu	Gly	Gly	Phe	Ser	Phe	Cys	Gln	Xaa	Arg		
			40					45				50				
ctc	aat	aag	cgc	aag	gaa	tac	atg	gtg	cgc	tagggccccg	gcgcgtttcc					403
Leu	Asn	Lys	Arg	Lys	Glu	Tyr	Met	Val	Arg							
			55					60								
ccgctccagc	ccctcctcta	tttaaaract	ccctgcaccg	tktcacccag	gtcgcgtccc											463
acccttgccg	gcgcctctctg	tgggactggg	tttcccgggc	rararactga	atcccttctc											523
ccatctctgg	catccggccc	ccgtggarar	ggctgaggct	ggggggctgt	tccgtctctc											583
cacccttcgc	tgtgtcccgt	atctcaataa	agagaatctg	ctctcttcaa	aaaaaaaaaa											643
my																645

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 seq FLPCCLLWSVFNP/ES

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 <222> 761..773

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 <223> n=a, g, c or t

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aaaacaattc	atgcctttca	tagttttatta	ttattaaagt	ctaaacaaaa	ttgcaatttc											60
ttaggtaacc	ttatatattac	aataaatgaa	gattaccctc	aaatgctaga	agctgtctag											120
gtccgctccg	tgtgtcagat	tttcctcaga	ttagatgtgc	caataaccaa	gtttattcag											180
taaacaactt	gtacttggtt	catctgggtt	tattactctc	acccataaac	agtaatgact											240
ctctgaccct	ctggaaatat	gtaatgcttc	caatcttgct	ttgtgtatct	catttaattt											300
gttataaggt	agtactgatt	ttagcatatt	a atg cga	ttt ctt cct	tgt tgt											352
			Met Arg Phe	Leu Pro Cys	Cys											
			-15		-10											
ttg ctt tgg	tct gtg ttc	aat cca	gag agc	tta aat	tgt cat	tat ttt										400
Leu Leu Trp	Ser Val Phe	Asn Pro	Glu Ser	Leu Asn	Cys His	Tyr Phe										

	-5		1		5			
ghk	ndd	gaa	amc	tgt	att	ttt	gyt agt tta caa tat tat gaa att tca	448
Xaa	Xaa	Glu	Xaa	Cys	Ile	Phe	Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser	
	10			15			20	
ctt	cag	gag	aaa	ctg	ctg	ggc	ttc ctg tgg ctt tgt ttt ctt agt tac	496
Leu	Gln	Glu	Lys	Leu	Leu	Gly	Phe Leu Trp Leu Cys Phe Leu Ser Tyr	
25			30			35	40	
ttt	ttc	cgt	gcc	gtg	tat	ttt	tta att gat ttt tct tct ttt act	541
Phe	Phe	Arg	Ala	Val	Tyr	Phe	Leu Ile Asp Phe Ser Ser Phe Thr	
	45			50			55	
tgaaaagaaa	gtgtttttatt	ttcaaattctg	gtccatatatt	acatttctagt	tcagagccaa			601
gccttaaaact	gtacagaatt	tccactgtaa	ttaaaactat	ttagtgtag	ttataaatag			661
ccttcaaaaa	gagagattct	ccattacacg	atcacctgca	tcacagccca	tggtgaatgt			721
atgtttctgc	atagcgaaat	aaaaatggca	aatgcactga	aaaaaaaaaa	aa			773

<210> 273
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<220>
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 <222> 555..566

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aacgagtgga	ggtgtggcta	gtggctgtga tgagataaat cc atg cat agc ctt	54
		Met His Ser Leu	
		-45	
ttc att gcg agc ttg aaa gtt ctt ttc tat tac agt ttt agc ttt agg			102
Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser Phe Ser Phe Arg			
-40	-35	-30	
ttt aat tgg ttc gac tgc ctt ctc cac aat ttg ggc gag aat ttc ctt			150
Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly Glu Asn Phe Leu			
-25	-20	-15	-10
agc ctt ctc agc aaa agt tgt tct gcg gac ccg tct ggg tca act ttc			198
Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser Gly Ser Thr Phe			
	-5	1	5
atg agg gac att gag aca aac aaa tgaaatatgg gttaaagtac tctgagcagc			252
Met Arg Asp Ile Glu Thr Asn Lys			
	10	15	
tacaaaaaga	araccagtct	atcctgctgg agacagtggc cacgtgaara aagagctctt	312
gcagtatgaa	agaccacatg	gaaagagagg ccacatggaa ccaacagtca gcaccttggg	372

ttcggacacg tgaaraaatt catctcarac tgtgtatcct aaatcaggca cttgctgaat	432
ctaactacat gagtggagacc agttgacaac acatggagca racatgagct gttctcagtg	492
artcctacac aaattcctga ctcacaacac tgtgagcaat aaaatggttg ttattttaag	552
ccaaaaaaaaaaaa	566

<210> 274
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 115..231

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 <222> 115..180
 <223> Von Heijne matrix
 score 5
 seq HLFVTWSSQRALS/HP

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 <222> 419..424

<220>
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 <222> 445..455

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aacctgccag tkatgcaaat gccaaaatgt gggatcatcat atagtatatatt tgaaaccttt	60
ctgaacatgt acaccaccca atgctagagg ctgacttgga aaccgggtggg tgca atg	117
	Met
ccc gag gct gtg gaa caa tca gcc cat ctc ttt gtg acc tgg agc agt	165
Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser Ser	
-20 -15 -10	
cag agg gcc ctc agt cac ccc gcc cca ttc ctc acc ara raa aar aat	213
Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys Asn	
-5 1 5 10	
cca ttt cta tgg aag ctc tgacgtaact tcagtgtttt ctacaatact	261
Pro Phe Leu Trp Lys Leu	
15	
cctcctgccc cgccccatta aaacagttct tttgttaaaa aatavcctaa tgggtccaact	321
ttgctgtctg ttcttccaaa tgtttataat acacattatt tataaatatg tctgtttggg	381
aagctaagaa caagctagtt tttaacaacac aaatggaaat aaatgcaatt attataaaaa	441
tycaaaaaaaaaaaaa	455

<210> 275
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<220>
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 <222> 232..384

<220>


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      seq FFLCAAFPLGAGV/KM

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<221> polyA_signal
<222> 650..655

<220>
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<222> 662..673

<400> 275
atttggcttg cagactgcct tctatcccag aacagctgag aaatctatga agctgagatt    60
ctgaaggacc cagcttaggt tcttccactt aggcctcaat tcccttcctt ttccaggggc    120
agccttagtt tcccatggcc ctgaaacaca cacatttccc ccttcctttc ccagaagcca    180
ctggccccc atagcaccca gtgcctcctt ttacaagtg gaagaactag g atg gct    237
                                     Met Ala

ttc caa agt ctt cta gaa atg aag ttc ttt ctg tgt gca gct ttc ccc    285
Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro
   -20               -15               -10

ctt gga gca gga gtg aag atg ttt cat tat ctt ggg cct ggg aaa cca    333
Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro
   -5               1               5               10

ctt cyy cag gct tct ccc tcc ccc cac ccc cat agg amc agg att tgg    381
Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp
      15               20               25

cct tagcttctgg gcctatcsgc tgccttcctt cttyttccta ccacctcttc    434
Pro

tgccttcctt trawctctgt tgggcttggg gatcttagtt ttcttttggt tatttcccat    494
ctcatttttt tcttctgggc agttttttta aggggggggt ttgtggtttt ttgtttttgt    554
tttgcttctg aaaaarcatt tgcctttcct cctctcccaa cataacaatc gtggtaacag    614
aatgcgactg ctgatttacc gatgtattta atgtaagtaa aaaaaggaaa aaaaraaaa    673

<210> 276
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<222> 143..427

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<222> 143..286
<223> Von Heijne matrix
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      seq FVILLLFIFTVVS/LV

<220>
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<222> 606..611

<220>

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<221> polyA_site
<222> 628..639

<400> 276
aatcgcttca gcagcatcct ctcagacaag agccactatt tctgattcag atcacctgtc      60
atcgaagttt aaagaagggg aaacaggaga cagaaataca ctgaaccaa aagattcaaa      120
agagcaagtg gaatctctaa ga atg gct tcc agc cac tgg aat gaa acc act      172
                Met Ala Ser Ser His Trp Asn Glu Thr Thr
                -45                                -40
acc tct gtt tat cag tac ctt ggt ttt caa gtt caa aaa att tac cct      220
Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro
                -35                                -25
ttc cat gac aac tgg aac act gcc tgc ttt gtc atc ctg ctt tta ttt      268
Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile Leu Leu Leu Phe
                -20                                -15                                -10
ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc ctt tat gaa gtg      316
Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe Leu Tyr Glu Val
                -5                                1                                5                                10
ctt gam wgc tgc tgc tgt gta aaa aac aaa acc gtg aaa gac ttg aaa      364
Leu Xaa Xaa Cys Cys Cys Val Lys Asn Lys Thr Val Lys Asp Leu Lys
                15                                20                                25
agt gaa ccc aac cct ctt ara akt atg atg gac aac atc aga aaa cgt      412
Ser Glu Pro Asn Pro Leu Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg
                30                                35                                40
gaa act gaa gtg gtc taacactcta taraaaatga acaaaatctc tgaaagcagc      467
Glu Thr Glu Val Val
                45
tcaacctctt ctgaraaaaa aaatatattc tgaggccaac tgttgctaca aaacaaattc      527
tgactgaatg gttaaaacat ttctagtara aggggaaaaa aaakttaaac atgcactgtt      587
tgtgtgtata sccatttcat taaatatata gtaaaactyc aaaaaaaaaa aa      639

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<222> 284..463

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<222> 284..379
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        seq TFINITLWLGLSLC/QR

<220>
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<222> 762..772

<400> 277
acagctgggg ctttgtcttc tttattgcta ggagaatgta gcaatagaag ttctcatcgc      60
cctgtattgc acttttgggt ttaaggactg gaccagagt tcctgaaagc caaactccat      120
aagctgctca gtaagttcca agcacatagc cggctkhggg atgcgattcg gtcgaggtct      180
gttgaatgaa ggtagacgca gcaggcagtt tgtccttacc agtgacctgg aagacgggtg      240
cacttctgta gtgagctcac ttaccttccc tgaatggtga ggc atg gat gaa tat      295

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[illegible]

Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met	
-40 -35 -30	
aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc	368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val	
-25 -20 -15	
ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa gcc	416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys Ala	
-10 -5 1 5	
ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg	464
Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa Ala Lys Pro Thr Leu	
10 15 20	
ccg gtt gca acc act act gcc car ccc acc ttc cct tgt cct gac tgt	512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys	
25 30 35	
ggc aaa acc ttt ggg cag gct gtt tct ctg arg cgg cac csc caa atr	560
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa Arg His Xaa Gln Xaa	
40 45 50	
cat gar gtc cgt gcc cct cct ggc acc ttc gcc tgc aca rad tgc ggt	608
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Xaa Cys Gly	
55 60 65 70	
cag gac ttt gct car gaa rca ggg ctg cat caa cac tac att cgg cat	656
Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln His Tyr Ile Arg His	
75 80 85	
gcc cgg ggg gga ctc tgagttcagc ttaagcctct ccacggtgac ggggtggctct	711
Ala Arg Gly Gly Leu	
90	
gtggctggta ggactcaccc atgatatggg gtgcaggaac tctggggggc ctgaaggatt	771
tgcttccttc ccctgggaag gcagagggct cttaataaag aggacccka agattcttaa	831
aaaaaaaa	840

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 seq NLPHLQVVGLTWG/HI

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<220>
 <221> polyA_site
 <222> 829..840

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ga atg tat gtd tgg ccc tgt gct gtg gtc ctg gcc cag tac ctt tgg	107

Met	Tyr	Val	Trp	Pro	Cys	Ala	Val	Val	Leu	Ala	Gln	Tyr	Leu	Trp		
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ttt	cac	aga	aga	tct	ctg	cca	ggc	aag	gcc	atc	tta	gag	att	gga	gct	155
Phe	His	Arg	Arg	Ser	Leu	Pro	Gly	Lys	Ala	Ile	Leu	Glu	Ile	Gly	Ala	
<div style="display: flex; justify-content: space-between;"> -65 -60 -55 </div>																
gga	gtg	agc	ctt	cca	gga	att	ttg	gct	gcc	aaa	tgt	ggg	gca	gaa	gta	203
Gly	Val	Ser	Leu	Pro	Gly	Ile	Leu	Ala	Ala	Lys	Cys	Gly	Ala	Glu	Val	
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ata	ctg	tca	gac	agc	tca	gaa	ctg	cct	cac	tgt	ctg	gaa	gtc	tgt	cgg	251
Ile	Leu	Ser	Asp	Ser	Ser	Glu	Leu	Pro	His	Cys	Leu	Glu	Val	Cys	Arg	
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caa	agc	tgc	caa	atg	aat	aac	ctg	cca	cat	ctg	cag	gtg	gta	gga	cta	299
Gln	Ser	Cys	Gln	Met	Asn	Asn	Leu	Pro	His	Leu	Gln	Val	Val	Gly	Leu	
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aca	tgg	ggg	cat	ata	tct	tgg	gat	ctt	ctg	gct	cta	cca	cca	caa	gat	347
Thr	Trp	Gly	His	Ile	Ser	Trp	Asp	Leu	Leu	Ala	Leu	Pro	Pro	Gln	Asp	
<div style="display: flex; justify-content: space-between;"> 1 5 10 </div>																
att	atc	ctt	gca	tct	gat	gtg	ttc	ttt	gaa	cca	gaa	rat	ttt	gaa	gac	395
Ile	Ile	Leu	Ala	Ser	Asp	Val	Phe	Phe	Glu	Pro	Glu	Xaa	Phe	Glu	Asp	
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Ile	Leu	Ala	Thr	Ile	Tyr	Phe	Leu	Met	His	Lys	Asn	Pro	Lys	Val	Gln	
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ttg	tgg	tct	act	tat	caa	ggt	agg	art	gct	gac	tgg	tca	ctt	gaa	gct	491
Leu	Trp	Ser	Thr	Tyr	Gln	Val	Arg	Xaa	Ala	Asp	Trp	Ser	Leu	Glu	Ala	
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tta	ctc	tac	aaa	tgg	gat	atg	aaa	tgt	gtc	cac	att	cct	ctt	gag	tct	539
Leu	Leu	Tyr	Lys	Trp	Asp	Met	Lys	Cys	Val	His	Ile	Pro	Leu	Glu	Ser	
<div style="display: flex; justify-content: space-between;"> 65 70 75 </div>																
ttt	gat	gca	gac	aaa	gaa	rat	ata	gca	gaa	tct	acc	ctt	cca	gga	aga	587
Phe	Asp	Ala	Asp	Lys	Glu	Xaa	Ile	Ala	Glu	Ser	Thr	Leu	Pro	Gly	Arg	
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cat	aca	ggt	gaa	atg	ctg	gtc	att	tcc	ttt	gca	aag	gac	agt	ctc		632
His	Thr	Val	Glu	Met	Leu	Val	Ile	Ser	Phe	Ala	Lys	Asp	Ser	Leu		
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tgaattatac	ctacaacctg	ttctgggaca	gtatcaatac	tgatgagcaa	cctggcacac											692
aaactatgag	cagaccactt	cagcttgaga	atgcagtggg	tctgaagatg	gtcaagtctg											752
tttgcccttar	atcttgatgt	cacctagaca	acacttaaac	tcatatgaaa	caaaaattaa											812
aatacgtatt	acaagcaaaa	aaaaaaaa														840

<210> 280

<211> 849

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..362

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<221> sig_peptide

<222> 21..200

<223> Von Heijne matrix

score 4.80000019073486

seq LVILSLKSQTLDA/ET

<220>

<221> polyA_signal
 <222> 821..826

<220>
 <221> polyA_site
 <222> 838..849

<400> 280

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agtaagtccc cccgcctcgc atg atg gct gcg gtg ccg ccg ggc ctg gag ccg      53
                        Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
                        -60                      -55                      -50

tgg aac cgt gtg aga atc cct aag gcg ggg aac cgc agc gca gtg aca      101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
                        -45                      -40                      -35

gtg cag aac ccc ggc gcg gcc ctt gac ctt tgc att gca gct gta att      149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
                        -30                      -25                      -20

aaa gaa tgc cat ctc gtc ata ctg tgc ctg aag agc caa acc tta gat      197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
                        -15                      -10                      -5

gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga      245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
      1              5              10              15

atg ggc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt      293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
                        20              25              30

tta aag cgt ttg aaa aac atg aat ttg gag ggc tca att caa gac ctg      341
Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu
                        35              40              45

ttt gag ttg ttt tct tcc aag taagtaagtg gtccarttgc tttgtgatgt      392
Phe Glu Leu Phe Ser Ser Lys
      50

ggtgggctgg gaactcaatg tcttgtgatc kcccttwgga ttkctctakg ctygckgttg      452
gaatataacc aattataaccw cagctgtaka aatwttgttt taatgtgggg taccygggtg      512
ktgtggtaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt      572
catggtagat tatattaaaa catcagtggg ctgttattgt gcttaactac ctcaagttga      632
gcttaaagca agtcttcact tgaaaactgc tatagaaatg ctttatattt aaaaatgaaa      692
gtaatgggar mttgcacata gctgaaaatg tgaagggtcg cccagggagg amatggaagc      752
tctgtgcttc ttctgccata ccttgcccta tgcattctct tgtttcaatc ctttgtcata      812
tcctttataa taaactggta aatgtaaaaa aaaaaaa      849

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<210> 281
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> 21..344
 <223> Von Heijne matrix
 score 5.30000019073486
 seq ACMTLTASPGVFP/SL

<220>
 <221> polyA_signal
 <222> 1305..1310

<220>
 <221> polyA_site
 <222> 1330..1341

<400> 281

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aaacaactcc ggaaagtaca atg acc agc ggg cag gcc cga gct tcc wyc cag      53
                        Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln
                        -105                      -100

tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat atc tca gtc tca      101
Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser
                        -95                      -90                      -85

atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc      149
Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg
                        -80                      -75                      -70

aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt      197
Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu
-65                      -60                      -55                      -50

tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct      245
Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro
                        -45                      -40                      -35

aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag      293
Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln
                        -30                      -25                      -20

gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc      341
Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe
                        -15                      -10                      -5

ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg      389
Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr
1                      5                      10                      15

cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa      437
Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln
                        20                      25                      30

aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg      485
Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu
                        35                      40                      45

gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag      533
Glu Lys Ser Ile Met Leu
50

atgatgaccg ttcattaata aatttgcac tcatgcacac cagttacttc ctctttgtga      593
tggtgataac aatgttttgc tatgctgtta tcaagggcag acctagcaaa ttgcgtcaga      653
gcaatcctga attttgtccc gagaagggtg ctttggctga agcctaattc cacagctcct      713
tgttttttga gagagactga gagaaccata atccttgcc tctgaaccca gctggggcct      773
ggatgctctg tgaatacatt atcttgcgat gttggggttat tccagccaaa gacatttcaa      833
gtgcctgtaa ctgatttgta catatttata aaaatctatt cagaaattgg tccaataatg      893
cacgtgcttt gccctgggta cagccagagc ccttcaaccc caccttggac ttgaggacct      953
acctgatggg acgtttccac gtgtctctag agaaggatcc tggatctagc tggtcacgac      1013
gatgttttca ccaaggtcac aggagcattg cgtcgctgat ggggttgaag tttggtttgg      1073
ttcttgtttc agcccaatat gtagagaaca tttgaaacag tctgcacctt tgatacggta      1133
ttgcatttcc aaagccacca atccattttg tggattttat gtgtctgtgg cttaataatc      1193
atagtaacaa caataatacc tttttctcca ttttgcttgc aggaacata ccttaagttt      1253
ttttgtttt gttttgtttt ttttgttttt tgttttcctt tatgaagaaa aaataaaaata      1313
gtcacatttt aatacyaaaa aaaaaaaamc h      1344

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<210> 282
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 <213> Homo sapiens

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 <222> 1..201

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 <222> 1..63
 <223> Von Heijne matrix
 score 5.09999990463257
 seq LLLKIWLLQRPES/QE

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 <222> 637..642

<220>
 <221> polyA_site
 <222> 660..671

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<400> 282
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Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
   -20                      -15                      -10
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg      96
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
   -5                      1                      5                      10
atg gag agg aga gtt aaa aat gac ctc atg tcc ttc ttg tcc acg gtt     144
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
           15                      20                      25
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca     192
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
           30                      35                      40
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtctttgg           241
Leu Arg Met
   45
ctcagttcat ttaaaaaaga tatctatattg aaagttctca rarttgtaca tatgtttcac    301
agtacaggat ctgtacataa aagttttcttt cctaaaccat tcaccaagag ccaatatcta    361
ggcattttct tggtagcaca aattttctta ttgcttaraa aattgtcctc cttgttattt    421
ctgtttgtaa racttaagtg agttaggtct ttaaggaaag caacgctcct ctgaaatgct    481
tgtctttttt ctgttgccga aatarctggg ccttttttcgg gagttaratg tatarartgt    541
ttgtatgtaa acatttcttg taggcatcac catgaacaaa gatatatattt ctatttattt    601
attatatgtg cacttcaaga agtcactgtc agagaaataa agaattgtct taaatgtcaa    661
aaaaaaaaaa                                     671

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<210> 283
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 <212> DNA
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 <222> 39..1034

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 <223> Von Heijne matrix
 score 6.09999990463257
 seq LPLLTSAHGLQQ/QH

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 <222> 1566..1571

<220>
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 <222> 1587..1597

<400> 283
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 Met Ile Xaa Leu Arg Asp
 -30
 aca gct gcc tcc ctc cgc ctt gag aga gac aca agg cag ttg cca ctg 104
 Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln Leu Pro Leu
 -25 -20 -15
 ctc acc agt gcc ctg cac gga ctg cag cag cag cca gcc ttc tct 152
 Leu Thr Ser Ala Leu His Gly Leu Gln Gln Gln His Pro Ala Phe Ser
 -10 -5 1 5
 ggt gtg gca cgg ctg gcc aag cgg tgg gtg cgt gcc cag ctt ctt ggt 200
 Gly Val Ala Arg Leu Ala Lys Arg Trp Val Arg Ala Gln Leu Leu Gly
 10 15 20
 gag ggt ttc gct gat gag agc ctg gat ctg gtg gcc gct gcc ctt ttc 248
 Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu Val Ala Ala Ala Leu Phe
 25 30 35
 ctg cac cct gag ccc ttc acc cct ccg agt tcc ccc cag gtt ggc ttc 296
 Leu His Pro Glu Pro Phe Thr Pro Pro Ser Ser Pro Gln Val Gly Phe
 40 45 50
 ctt cga ttc ctt ttc ttg gta tca acg ttt gat tgg aag aac aac ccc 344
 Leu Arg Phe Leu Phe Leu Val Ser Thr Phe Asp Trp Lys Asn Asn Pro
 55 60 65 70
 ctc ttt gtc aac ctc aat aat gag ctc act gtg gag gag cag gtg gar 392
 Leu Phe Val Asn Leu Asn Asn Glu Leu Thr Val Glu Glu Gln Val Glu
 75 80 85
 atc cgc agt ggc ttc ctg gca gct cgg gca cag ctc ccc gtc atg gtc 440
 Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala Gln Leu Pro Val Met Val
 90 95 100
 att gtt acc ccc caa rac cgc aaa aac tct gtg tgg aca cag gat gga 488
 Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser Val Trp Thr Gln Asp Gly
 105 110 115
 ccc tca gcc car atc ctg cag cag ctt gtg gtc ctg gca gct gaa scc 536
 Pro Ser Ala Gln Ile Leu Gln Gln Leu Val Val Leu Ala Ala Glu Xaa
 120 125 130
 ctg ccc atg tta rar aas cag ctc atg gat ccc cgg gga cct ggg gac 584
 Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp Pro Arg Gly Pro Gly Asp
 135 140 145 150
 atc agg aca gkg ttc cgg ccg ccc ttg gac att tac gac gtg ctg att 632
 Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp Ile Tyr Asp Val Leu Ile
 155 160 165
 cgc ctg tct cct cgc cat atc ccg cgg cac cgc cag gct gtg gac tcr 680

Arg	Leu	Ser	Pro	Arg	His	Ile	Pro	Arg	His	Arg	Gln	Ala	Val	Asp	Ser		
			170					175					180				
cca	gct	gcc	tcc	ttc	tgc	cgg	ggc	ctg	ctc	agc	cag	ccg	ggg	ccc	tca	728	
Pro	Ala	Ala	Ser	Phe	Cys	Arg	Gly	Leu	Leu	Ser	Gln	Pro	Gly	Pro	Ser		
			185				190					195					
tcc	ctg	atg	ccc	gtg	ctg	ggc	tak	gat	cct	cct	cag	ctc	tat	ctg	acg	776	
Ser	Leu	Met	Pro	Val	Leu	Gly	Xaa	Asp	Pro	Pro	Gln	Leu	Tyr	Leu	Thr		
		200				205					210						
cag	ctc	arg	gag	gcc	ttt	ggg	gat	ctg	gcc	ctt	ttc	ttc	tat	gac	cag	824	
Gln	Leu	Xaa	Glu	Ala	Phe	Gly	Asp	Leu	Ala	Leu	Phe	Phe	Tyr	Asp	Gln		
		215			220				225					230			
cat	ggt	gga	gag	gtg	att	ggt	gtc	ctc	tgg	aag	ccc	acc	agc	ttc	cag	872	
His	Gly	Gly	Glu	Val	Ile	Gly	Val	Leu	Trp	Lys	Pro	Thr	Ser	Phe	Gln		
			235				240						245				
ccg	cag	ccc	ttc	aag	gcc	tcc	agc	aca	aag	ggg	cgc	atg	gtg	atg	tct	920	
Pro	Gln	Pro	Phe	Lys	Ala	Ser	Ser	Thr	Lys	Gly	Arg	Met	Val	Met	Ser		
			250				255					260					
cga	ggt	ggg	gag	cta	gta	atg	gtg	ccc	aat	gtt	gaa	gca	atc	ctg	gag	968	
Arg	Gly	Gly	Glu	Leu	Val	Met	Val	Pro	Asn	Val	Glu	Ala	Ile	Leu	Glu		
		265				270					275						
gac	ttt	gct	gtg	ctg	ggt	gaa	ggc	ctg	gtg	cag	act	gtg	gag	gcc	cga	1016	
Asp	Phe	Ala	Val	Leu	Gly	Glu	Gly	Leu	Val	Gln	Thr	Val	Glu	Ala	Arg		
		280				285				290							
agt	gag	agg	tgg	act	gtg	tgatcccagc	tctggagcaa	gctgtagacg								1064	
Ser	Glu	Arg	Trp	Thr	Val												
		295			300												
gacagcagg	gacatgaatc	cattggacct	ctagagcaag	atgtcagtag	gatgacctcc	accctccttg	1124										
		ctccatggag	ggcctgctgg	ctgaacatgc	tgaatcatct	ccaacaaaac	1184										
		ctttctctct	gatgtccag	cattggggca	ggggcatggt	ggcccatgta	1244										
		cctcaccatc	ccagaagagg	agtgggagcc	agctcagaga	aggaactgaa	1304										
		ccatccacct	attagccctg	ggcctggacc	tccctgcgat	ttccactcc	1364										
		ttctttagtc	ttcttccaga	aacagagaag	gggatgtgtg	cctgggagag	gctctgtctc	1424									
		cttcctgctg	ccaggacctg	tgccctagact	tagcatgccc	ttcactgcag	tgtcaggcct	1484									
		ttagatggga	cccagcgaaa	atgtggccct	tctgagtcac	atcaccgaca	ctgagcagtg	1544									
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<210> 284

<211> 1206

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<222> 69..263

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<221> sig_peptide

<222> 69..125

<223> Von Heijne matrix
score 3.90000009536743
seq ALSMSSFSFHSSS/CS

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<221> polyA_signal

<222> 1173..1178

<220>

<221> polyA_site

<222> 1196..1205

<400> 284

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acatttgatga ctttaccaat accctcccag ttcttgatag acagctgtag gttgctgggt      60
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt      110
      Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser
            -15                               -10

ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc      158
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser
-5              1              5              10

aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta      206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu
            15              20              25

gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa      254
Glu Asn Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys
            30              35              40

att gtg ggc tgatttggtc ttctctctct cctcccactg ttactgcctt      303
Ile Val Gly
      45

gcagcccttg ttcaggtgta cagaccctta ttctggcctc tagtgtcctt gtctgtcatg      363
acacaccctt ccgccc aaat acctctgacc ccaaggctgg aatggggctg gtaggarata      423
agtttgctta ctcatartca tgtcctttct cttggcacct gcttccctgc ggtgtcctca      483
aatggatttc tgtgtggcag tggartgatt gcatgaattt ttctgtaaca cattaacttt      543
gtattattat taagggartt tgaraaagct ttgcttataa tgtcaaggca aggaggtaaa      603
aactggagcc caaakaaatt cccttagggc aagattatgt tataataaraa aattgaattt      663
cctgaggcag tggctgccac cccttttcar atgttttagtc ctgcaaatac catctttctt      723
gtagtctgtg acatggatgg ggatgctagg gcccttaggg gcaaggggac taaactaaat      783
caakttgagt ttttttccag caggggttar gggaggtagt cscgtttgat atttgacact      843
araaagtaat cttttttaca aaactgtttt tctaggtggg tggaaagtga aactgccaca      903
tccttgttgg tttagtccaa raratcattt gcaacaacag taratgtccg ggttttgttt      963
ctgtcttttt attatgaaaa actatgttaa ggggggaaat gtggattatg gtaaccarag     1023
gaatccctas ccttgttttc cttaraarac ttgttttagtg ttttatcara cgtctgttgt     1083
agttgtarac aggaaagctt gtgaraaaaa caccacatgg ascctgtaaa tgtttttgca     1143
caacctgtaa agcattcttg gaaktggcca gtaaaaaggg gtttttaccat ttaaaaaaaa     1203
aat                                                                 1206
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<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..285

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<221> sig_peptide

<222> 115..204

<223> Von Heijne matrix

score 3.70000004768372

seq SMMLLTVYGGYLC/SV

<220>

<221> polyA_signal

<222> 505..510

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<220>
<221> polyA_site
<222> 525..536

<400> 285
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tgcctgagga ggcctcgggt ggatgcgaag gagctgcagc atccagggga caag atg      117
                                         Met
                                         -30
cca act ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc      165
Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr
          -25          -20          -15
tcc atg atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga      213
Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val Arg
          -10          -5          1
gtc tac cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa      261
Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala Glu
      5          10          15
gaa cag aag dac tca gga atc atg tagaactggg gggctttttc tctgagcar      315
Glu Gln Lys Xaa Ser Gly Ile Met
20          25
asakgcccaa ggcattgtgt ggagagactt cacctgccac catttccagg tcaacaggac      375
tagagcgttg atggttttca aaccctgttg gaagaaagtg cccatggttt ctctggttct      435
gccartttga cagtttatgg argcttttga atcgtaatar caatgtgagg gtgargtaca      495
cctacagaca ttaaataatt tgctgtgtca aaaaaaaaaa a      536

<210> 286
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..344

<220>
<221> sig_peptide
<222> 90..140
<223> Von Heijne matrix
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      seq LLLITAILAVAVG/FP

<220>
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<222> 500..505

<220>
<221> polyA_site
<222> 515..527

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gagagaaaga actgactgar acgttttgag atg aag aaa gtt ctc ctc ctg atc      113
                                         Met Lys Lys Val Leu Leu Leu Ile
                                         -15          -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag      161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln

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	-5	1	5	
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr				209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly				
	10	15	20	
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att				257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile				
	25	30	35	
cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata				305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile				
	40	45	50	55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa				354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys				
	60	65		
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat				414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta				474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aaacc				529

<210> 287
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 57..311

<220>
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 <222> 57..107
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLLITAILAVAVG/FP

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 <222> 482..493

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aag aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt	107
Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly	
	-15 -10 -5
ttc cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac	155
Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp	
	1 5 10 15
agc gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca	203
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro	
	20 25 30
ttt cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga	251
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg	
	35 40 45
cgt aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt	299

Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu
 50 55 60
 ccg agc gaa aag taaacaagaa ggaaaagtca cgataaacct ggtcacctga 351
 Pro Ser Glu Lys
 65
 aattgaaatt gagccacttc cttgargaat caaaattcct gttaataaaa gaaaaacaaa 411
 tgtaattgaa atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa 471
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 <210> 288
 <211> 521
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 96..302

 <220>
 <221> sig_peptide
 <222> 96..182
 <223> Von Heijne matrix
 score 5
 seq ELSLLPSSLWVLA/TS

 <220>
 <221> polyA_site
 <222> 501..514

 <400> 288
 aagagacgtc accggctgcg cccttcagta tcgcgagcgg aagatggcgt ccgccaccgc 60
 tctcatccag cggctgcgga actgggcgtc cgggc atg acc tgc agg gga agc 113
 Met Thr Cys Arg Gly Ser
 -25
 tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca 161
 Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro
 -20 -15 -10
 agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca 209
 Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala
 -5 1 5
 ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt 257
 Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg
 10 15 20 25
 crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg 302
 Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Gln Xaa Ala Leu Leu
 30 35 40
 tagctgccac tgaaaaraag gcggtgactc cagctcctcc cataaagagg tgggagctgt 362
 cctcggacca gccttacctg tgacactgca ccctcacggc caccgacta ctttgctcctc 422
 ttggatttcc tccagggaga atgtgacctt atttatgaca aatacgtara gctcaggtat 482
 cacttctagt ttactttaaa aaaataaaaa aatagagac 521

 <210> 289
 <211> 811
 <212> DNA
 <213> Homo sapiens

 <220>

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<221> CDS
<222> 161..526

<220>
<221> sig_peptide
<222> 161..328
<223> Von Heijne matrix
      score 4.19999980926514
      seq XSPLLTLALLGQC/SL

<220>
<221> polyA_site
<222> 799..811

<220>
<221> misc_feature
<222> 156
<223> n=a, g, c or t

<400> 289
aaaaaattgc agtgctgaag acactggacc cgcaaaaggc tgtccctccc aaacctggga      60
ttctgggctc actgagttca cctgcgagtc agccctacct gcaactgctct ggtctagtag      120
aaacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc      175
                                         Met Val Pro Trp Pro
                                         -55
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc      223
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe
      -50                      -45                      -40
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct      271
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser
      -35                      -30                      -25                      -20
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg      319
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu
                      -15                      -10                      -5
ggt cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa      367
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln
                      1                      5                      10
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg      415
Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp
      15                      20                      25
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaa      463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys
      30                      35                      40                      45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt      511
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val
                      50                      55                      60
caa ttt ttt tta ggg tgaatggagg garagttggg gactgaaaas ccttcaaara      566
Gln Phe Phe Leu Gly
                      65
caatgttatt acagcaktct ccccttatcc aaaktttcct tttcctgadt ttcagttagc      626
tatgggtcaac cgcttggaac atakttgaac acagtacaat aaratatttt gaggctggga      686
ktgggtggctc atgcctgtaa taatcccagg actttgtgar accaaktttg aaggatcact      746
tgaaccaggg aktttgarac cascctgggc aacatrgtra gacctcatct ctacaaaaaa      806
aaaaa                                         811

<210> 290
<211> 625

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..332

<220>
<221> sig_peptide
<222> 210..299
<223> Von Heijne matrix
score 8.10000038146973
seq ITCLLAFWVPASC/IQ

<220>
<221> polyA_signal
<222> 594..599

<220>
<221> polyA_site
<222> 613..625

<400> 290
acaggtcsmc ttaacatctc ttgatttgag ccactccac tgatcatcagc ttccacctgg 60
attatcgtga cagcctccta ctgcttctct atcatgtggc cagagctatc ttccctaaaa 120
atgcattgca tagttgatca agtcactctc tggcctaaaa ccttccttgg ctccctgctg 180
ccctcaggat aaagtctgga cccctcagc atg gct tgt gag act cat ggt gtc 233
Met Ala Cys Glu Thr His Gly Val
-30 -25
ctt gtc cct gct cac ctg tct ggt ctg atc act tgc ctt ctt gca ttc 281
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe
-20 -15 -10
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca 329
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro
-5 1 5 10
ctc tgattcctcc tttcttttgg tcacagagaa aggggtacttt ctctgtcaaa 382
Leu
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgaccccc 442
accctggcat actacacara tcactctggg ctactttgcc tgcctaattg tcactctccc 502
agtaaactgt aagctccttg agggcaagga ttgtgttggc atttttgtat taacagtgcc 562
tggcttgggtg cctggcacct aaaaagcact caataaatgt ttgtttaatg aaaaaaaaaa 622
aaa 625

<210> 291
<211> 684
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..361

<220>
<221> sig_peptide
<222> 212..319
<223> Von Heijne matrix
score 4.09999990463257

seq HWLFLASLSGIKT/YQ

<220>

<221> polyA_signal

<222> 650..655

<220>

<221> polyA_site

<222> 673..684

<220>

<221> misc_feature

<222> 9,571

<223> n=a, g, c or t

<400> 291

atccccawns	cactctctca	cagagactgt	tcttttcctt	ctgagaccct	actccagctt	60
gtagttctaa	atctgtgatt	atgcactgtc	tgtcttcctc	ttgaggtcag	gggccatttc	120
ttttgttctc	tgctatgtc	aggaccaga	tcaaaggagc	tcagtaacta	tttacaggcg	180
tacatcatat	gtggaggaca	cttatgtctg	g atg gcc cca cac aca gct tcc			232

Met Ala Pro His Thr Ala Ser

-35

-30

ttt ggg gtc tgt ccc ctg ctc tcc gtt acc cgc	gtg gta gcc act gag	280
Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg	Val Val Ala Thr Glu	

-25

-20

-15

cac tgg ctc ttc ctg gct tca ctc tct ggc atc	aaa act tat cag tcc	328
His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile	Lys Thr Tyr Gln Ser	

-10

-5

1

tac atc tca gtc ttt tgc aag gtg aca ctt atc	tgattaccta attcacacra	381
Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile		

5

10

aggtgttaat	ggtggtaatg	gcataktatt	tattacccca	ggggaccak	aacggtggta	441
tcaaaacata	tcattcccca	gtgggtttaa	actctggtag	ctttccargg	aatccaaagt	501
ggaatccagt	ctccttagct	gawttcacag	ggccccgtct	gcacaacttg	gcttctgtcg	561
gcttccctan	ccctgacttc	ccaagcctta	gtcatcaccc	tctctcccac	ccagggtcca	621
gcacagtacc	tggaacagtc	aagccctcaa	taaatgttta	ctgagtgcac	yaaaaaaaaa	681
aaa						684

<210> 292

<211> 628

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 75..482

<220>

<221> sig_peptide

<222> 75..128

<223> Von Heijne matrix

score 3.59999990463257

seq KMLISVAMLGAXA/GV

<220>

<221> polyA_signal

<222> 595..600

<220>
 <221> polyA_site
 <222> 618..627

<220>
 <221> misc_feature
 <222> 434
 <223> n=a, g, c or t

<400> 292
 aagtgaagacc ggcgcggcaac agcttgccggc tgcgggggagc tcccgtgggc gctccgctgg 60
 ctgtgcaggc ggcc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca 110
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
 -15 -10
 atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg 158
 Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
 -5 1 5 10
 acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg 206
 Thr Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
 15 20 25
 cag gac cca agg agc agg gag gag gcg gcc agg acc cag cag cta ttg 254
 Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 30 35 40
 ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg 302
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
 45 50 55
 agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac 350
 Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His
 60 65 70
 cgt gag acc gga ctt gcc tcc gtg ggc gcc gga cct tgg ctt ggg cgc 398
 Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
 75 80 85 90
 agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg 446
 Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
 95 100 105
 amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg 492
 Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
 110 115
 tcgggtgagc acgtgtcccc caaacctgg actgactgct ttaagggtccg caaggcgggc 552
 cagggccgag acgcgagtcg gatgtggtga actgaaagaa ccaataaaat catgttcctc 612
 cammcaaaaa aaaaah 628

<210> 293
 <211> 813
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 50..631

<220>
 <221> sig_peptide
 <222> 50..244
 <223> Von Heijne matrix
 score 8

seq LTLIGCLVTGVES/KI

<220>

<221> polyA_signal

<222> 777..782

<220>

<221> polyA_site

<222> 801..812

<400> 293

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aaggaaagga ttactcgagc cttgttagaa tcagacatgg cttcagggg atg cag gac      58
                                   Met Gln Asp
                                   -65
gct ccc ctg agc tgc ctg tca ccg act aag tgg agc agt gtt tct tcc      106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
      -60                                -55                                -50
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg      154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
      -45                                -40                                -35
cct ttt cag ttc tgt ctc cgg cag gct ttg agg atg aag gct gcg ggc      202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
      -30                                -25                                -20                                -15
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc      250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
      -10                                -5                                1
tac act cgt tgc aaa ctg gca aaa ata ttc tgc agg gct ggc ctg gac      298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
      5                                10                                15
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat      346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr
      20                                25                                30
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc      394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser
      35                                40                                45                                50
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc      442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg
      55                                60                                65
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg      490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu
      70                                75                                80
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt      538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val
      85                                90                                95
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt      586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys
      100                                105                                110
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc      631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser
      115                                120                                125
taaactggaa ctggaccag gatgctttgc ascaacgccc tagggtttgc agtgaatgtc      691
caaatgcctg tgtcatcttg tcccgtttcc tcccaatatt ccttctcaaa cttggagagg      751
gaaaattaag ctatactttt aagaaaataa atatttccat ttaaatgtca amaaaaaaaa      811
ah                                                                    813

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<210> 294

<211> 778

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..576

<220>
 <221> sig_peptide
 <222> 154..360
 <223> Von Heijne matrix
 score 4.80000019073486
 seq MMVLSLGIILASA/SF

<220>
 <221> polyA_signal
 <222> 737..742

<220>
 <221> polyA_site
 <222> 763..775

<400> 294
 agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga 60
 aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag 120
 ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc 174
 Met Thr Ser Gln Pro Val Pro
 -65
 aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 222
 Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
 -60 -55 -50
 gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 270
 Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
 -45 -40 -35
 cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt 318
 His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
 -30 -25 -20 -15
 ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 366
 Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
 -10 -5 1
 tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 414
 Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
 5 10 15
 cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg 462
 Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg
 20 25 30
 atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct 510
 Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa
 35 40 45 50
 gcc agc ttg cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa 558
 Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu
 55 60 65
 tct tgt tct cct gtc ggg targataaca ggggttgctt ratttttagat 606
 Ser Cys Ser Pro Val Gly
 70
 caattttctta tcagactcaa ataaacattt cttttgaaaa tcatcttatt cttcacatta 666
 tcatcttgag ctatgatgga aactagtgas ktctctccag gtttaggcga aaaaaaatc 726

catgaattag gataaagttg ggaaggaaca ttttatacaa aaaaaaaaaah cc

778

<210> 295

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 154..897

<220>

<221> sig_peptide

<222> 154..360

<223> Von Heijne matrix
score 4.80000019073486
seq MMVLSLGIILASA/SF

<220>

<221> polyA_signal

<222> 1017..1022

<220>

<221> polyA_site

<222> 1044..1054

<220>

<221> misc_feature

<222> 1058

<223> n=a, g, c or t

<400> 295

agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga	60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag	120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc	174
Met Thr Ser Gln Pro Val Pro	
-65	
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa	222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln	
-60 -55 -50	
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa	270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys	
-45 -40 -35	
cat cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt	318
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys	
-30 -25 -20 -15	
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc	366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe	
-10 -5 1	
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac	414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr	
5 10 15	
cca ttc ata gga ccc ttt ttt ttt atc atc tct ggc tct cta tca atc	462
Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile	
20 25 30	
gcc aca aaa aaa agg tta acc aac ctt ttg gtg cat acc acc ctg gtt	510
Ala Thr Lys Lys Arg Leu Thr Asn Leu Leu Val His Thr Thr Leu Val	

35	40	45	50	
gga agc att ctg agt gct ctg tct gcc ctg gtg ggt ttc att ayc ctg				558
Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Xaa Leu				
	55	60	65	
tct gtc aaa cag gcc acc tta aat cct gcc tca ctg cak tgt gag ttg				606
Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Xaa Cys Glu Leu				
	70	75	80	
gmc aaa aat aat ata cca aca ara akt tat gtt yct tac ttt tat cat				654
Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa Tyr Val Xaa Tyr Phe Tyr His				
	85	90	95	
gat tca ctt tat acc acg gac kgc tat aca gcc aaa gcc akt ctg gct				702
Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr Thr Ala Lys Ala Xaa Leu Ala				
	100	105	110	
gga act ctc tct ctg atg ctg att tgc act ctg ctg gaa ttc tgc cwa				750
Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Xaa				
	115	120	125	130
sct gtg ctc act gct gtg ctg cgg tgg aaa cag gct tac tct gac ttc				798
Xaa Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe				
	135	140	145	
cct ggg agt gta ctt ttc ctg cct cam agt tac att ggw aat tct ggm				846
Pro Gly Ser Val Leu Phe Leu Pro Xaa Ser Tyr Ile Gly Asn Ser Gly				
	150	155	160	
atg tcc tca aaa atg acy cat gac tgt gga tat gaa gaa cta ttg act				894
Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr				
	165	170	175	
tct taagaaaaaa gggagaaata ttaatcagaa agttgattct tatgataata				947
Ser				
tggaagagtt aaccattata gaaaagcaaa gcttgagttt cctaaatgta agctttttaa				1007
gtaatgaaca ttaaaaaaaa ccattatttc actgtcaaaa aaaaaaamcc nkt				1060

<210> 296
 <211> 444
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 146..292

<220>
 <221> sig_peptide
 <222> 146..253
 <223> Von Heijne matrix
 score 5.5
 seq FTSMCILFHCLLS/FQ

<220>
 <221> polyA_signal
 <222> 395..400

<220>
 <221> polyA_site
 <222> 433..444

<400> 296
 aacttgggac aagaratcaa acttttaaaga tgggtctaaag cccctcttaa aggtctgact 60
 gtgtcggacc tctagagcta atctcactag atgtgagcca ttgtttatat tctagccatc 120

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ctttcatttc attctagaag accccc atg caa gtt ccc cac cta agg gtc tgg      172
                               Met Gln Val Pro His Leu Arg Val Trp
                               -35                               -30
aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca      220
Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
      -25                               -20                               -15
agt atg tgc ata ttg ttc cac tgt ctt ctt agc ttt cag gtt ttc aaa      268
Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
      -10                               -5                               1                               5
aag aaa aga aaa ctt ara ctt ttc tgatgttctt ttttacgtaa ataaccattt      322
Lys Lys Arg Lys Leu Xaa Leu Phe
                               10
tattgttggt ttgctttttc tgccttcaaa ctactcccac aggccaaata tavctggctg      382
cttctttctg taaataaagt tttattgggc cacagccatg gccatctttt aaaaaaaaaa      442
aa                                                                444

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<210> 297
<211> 754
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 126..383

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<220>
<221> sig_peptide
<222> 126..167
<223> Von Heijne matrix
      score 7.5
      seq VALNLLILVPCCAA/WC

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<220>
<221> polyA_signal
<222> 726..731

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<220>
<221> polyA_site
<222> 743..754

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<400> 297
aattgtatgt tacgatgttg tattgatttt taagaaagta attkratttg taaaacttct      60
gctcgtttac actgcacatt gaatacaggt aactaattgg wgggagaggg gaggtcactc      120
ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg      170
      Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp
                               -10                               -5                               1
tgt gac cca cgg agg atc cac tcc cag gat gac gtg ctc cgt agc tct      218
Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser
      5                               10                               15
gct gct gat act ggg tct gcg atg cag cgg cgt gag gcc tgg gct ggt      266
Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly
      20                               25                               30
tgg aga agg tca caa ccc ttc tct gtt ggt ctg cct tct gct gaa aga      314
Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg
      35                               40                               45
ctc gag aac caa cca ggg aag ctg tcc tgg agg tcc ctg gtc gga gag      362
Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu

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50          55          60          65
gga cat aga atc tgt gac ctc tgacrrctgt gaasccaccc tgggctacar 413
Gly His Arg Ile Cys Asp Leu
70
aaaccacagt cttcccagca attattacaa ttcttgaatt ccttggggat tttttactgc 473
cctttcaaag cacttaaktg tkrratctaa cgtkttccag tgtctgtctg aggtgactta 533
aaaaatcaga acaaaaacttc tattatccag agtcatggga gagtacaccc tttccaggaa 593
taatgttttg ggaaacactg aaatgaaatc ttcccagtat tataaattgt gtatttataaa 653
aaaagaaact tttctgaatg cctacctggc ggtgtatacc aggcagtgtg ccagtttataa 713
aagatgaaaa agaataaaaa cttttgagga aaaaaaaaaa a 754

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tctcc atg acc cgg ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg 110
      Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro
          -55          -50          -45
atc cca gtt cct cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt 158
Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser
          -40          -35          -30
cca gtg cgt cca cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc 206
Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu
          -25          -20          -15
ctg gac agt gtc cta tgg ctg ggg gca cta gga ctg aca atc cag gca 254
Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala
          -10          -5          1          5
gtc ttt tcc acc act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc 302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe
          10          15          20

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ctc acc ttt gac ctg ctc cat agg ccc gca gtc aca ctc tgc cac agc	350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser	
25 30 35	
gca aac ttc tca cca ggg gcc aga gtc agg ggg ccg gtg aag gtc ctg	398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu	
40 45 50	
gac agc agg agg ctc tac tcc tgc aaa tgg gta cag tct cag gac aac	446
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn	
55 60 65	
tta gcc tcc agg aag cac tgc tgc tgc tgc tca tgg ggc tgg gcc cgc	494
Leu Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg	
70 75 80 85	
tcc tgaaaacctg tggcatgccc ttgwaccctg cttggcctgg ctttctgcct	547
Ser	
ccatccttgg gcctgakanc cctccccac aactcagtgt ccttcaaata tacaatgacc	607
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Met Glu Arg	
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ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc	105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly	
-10 -5 1	
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag	153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys	
5 10 15	
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac	201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp	
20 25 30 35	
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt agt gag tcy ccc	249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser Glu Ser Pro	
40 45 50	

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ccg ggc aga ggg cas gtg cca bgt gcc ggg gaa kgg ccg gtg ccc ccg      297
Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro Val Pro Pro
      55      60      65
cct ctc wkc gac tta bct atg act cct cgg ckc ycc agg gcc tgg ggc      345
Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg Ala Trp Gly
      70      75      80
cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tcg      393
Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser
      85      90      95
ggc gag cat ccs rva btg tgaatkkkga cttttttctc ckccatttga      441
Gly Glu His Pro Xaa Xaa
100      105
agtgtcacta ggaactgtca gcaggacaaa ggctctgatg tcactgaatt tacaaaraca      501
gcaggaacrs ackggtgggg atgggcagct gtterargcr atggggtkac tgcccttcct      561
ggcacagcac artacacctg ccatacaacc carcatcagg cakgctgcac tggaatcgat      621
acagtgtatg acaatgtcat atagtataac acaacataat gaatataacg tgtatattgc      681
aacttaatat aatacgatgt aatataatgc tacataatac aacataatat aataaaatag      741
aatgcaacac aaaaaaaaaa aacc      765

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                                   -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10      -5      1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5      10      15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
      20      25      30      35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta      249

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Gln	Val	Cys	Ile	Ser	Asn	Glu	Val	Val	Val	Ser	Phe	Lys	Trp	Ser	Val		
				40					45					50			
cgc	gtc	ctg	ctc	agc	aaa	cgc	tgt	gct	ccc	aga	tgt	ccc	aac	gac	aac	297	
Arg	Val	Leu	Leu	Ser	Lys	Arg	Cys	Ala	Pro	Arg	Cys	Pro	Asn	Asp	Asn		
				55				60					65				
atg	aak	ttc	gaa	tgg	tcg	ccg	gcc	ccc	atg	gtg	caa	ggc	gtg	atc	acc	345	
Met	Xaa	Phe	Glu	Trp	Ser	Pro	Ala	Pro	Met	Val	Gln	Gly	Val	Ile	Thr		
		70					75				80						
agg	cgc	tgc	tgt	tcc	tgg	gct	ctc	tgc	aac	agg	gca	ctg	acc	cca	cag	393	
Arg	Arg	Cys	Cys	Ser	Trp	Ala	Leu	Cys	Asn	Arg	Ala	Leu	Thr	Pro	Gln		
	85					90				95							
gag	ggg	cgc	tgg	gcc	ctg	cra	ggg	ggg	ctc	ctg	ctc	cag	gac	cct	tcg	441	
Glu	Gly	Arg	Trp	Ala	Leu	Xaa	Gly	Gly	Leu	Leu	Leu	Gln	Asp	Pro	Ser		
100					105				110					115			
agg	ggc	ara	aaa	acc	tgg	gtg	cgg	cca	cag	ctg	ggg	ctc	cca	ctc	tgc	489	
Arg	Gly	Xaa	Lys	Thr	Trp	Val	Arg	Pro	Gln	Leu	Gly	Leu	Pro	Leu	Cys		
				120				125					130				
ctt	ccc	awt	tcc	aac	ccc	ctc	tgc	cca	rgg	gaa	acc	cag	gaa	gga		534	
Leu	Pro	Xaa	Ser	Asn	Pro	Leu	Cys	Pro	Xaa	Glu	Thr	Gln	Glu	Gly			
			135					140					145				
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taaactctca	tgcccccaaa	aaaaaaaaaa														623	

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					Met	Xaa	Leu	Met	Val	Leu	Val	Phe	Thr				
					-20				-15								
att	ggg	cta	act	ttg	ctg	cta	gga	rtt	caa	gcc	atg	cct	gca	aat	cgc	160	
Ile	Gly	Leu	Thr	Leu	Leu	Leu	Gly	Xaa	Gln	Ala	Met	Pro	Ala	Asn	Arg		
	-10					-5			1					5			
ctc	tct	tgc	tac	aga	aag	ata	cta	aaa	gat	cac	aac	tgt	cac	aac	ctt	208	
Leu	Ser	Cys	Tyr	Arg	Lys	Ile	Leu	Lys	Asp	His	Asn	Cys	His	Asn	Leu		

	10	15	20	
ccg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat				256
Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp				
	25	30	35	
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc				304
His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe				
	40	45	50	
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat				352
Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp				
	55	60	65	
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct				400
Leu Phe Arg Asp Ser Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser				
	70	75	80	85
ggc gaa cac cat tcc tgatttccca caaactgcac tacatcagta taactgcatt				455
Gly Glu His His Ser				
	90			
tctagtttct atagagtgc atagagcata gattctataa attcttactt gtctaagaaa				515
gtaaatctgt gttaaacaag tagtaataaa agttaattca atccaaaaaa aaaaaa				571
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seq LLTHNLLSSHVRG/VG				
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			Met	
			-15	
aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg				106
Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly				
	-10	-5	1	
tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc				154
Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys				
	5	10	15	
cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg				202
Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val				
	20	25	30	
gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag				250

Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln	
35 40 45 50	
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Val Pro Arg Arg Ala Gly	
55	
gaggaccatg caccacctgc tgctggaggt ggamstgaka gagggcaccg tgcagtgcc	358
ggaatctgga cgtatgttcc ccatcagccg cgggatcccc aacatgctgc tgagtgaaga	418
ggaaactgag agttgattgt gccaggcgcc agtttttctt gttatgactg tgtatttttg	478
ttgatctata ccctgtttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac	538
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caaaaaaaaa aaaa	612
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seq FFIFCSLNTLLLG/GV	
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Met Lys Ser Ala Lys Leu Gly	
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ttt ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg	100
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu	
-15 -10 -5	
ggt ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat	148
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp	
1 5 10 15	
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt	196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe	
20 25 30	
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc	244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe	
35 40 45	
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt	292
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg	
50 55 60	
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg	338
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg	

65	70	75	
tgaactcatg aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcaractg	398		
attttwaaaat ctttgttwtat tttccmymak ggcgwktaag cttccatatg tttgctatgt	458		
tcctgaccct agttttgtct ttccctggaaa ttaactgtat gakcattasa atgaaagagt	518		
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ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat	101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp	
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tgc act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac	149
Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr	
5 10 15	
caa cgc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc	197
Gln Arg Phe Phe Ala Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr	
20 25 30	
tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag	245
Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln	
35 40 45 50	
ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc	293
Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys	
55 60 65	
tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act	341
Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr	
70 75 80	

cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt	389
His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys	
85 90 95	
tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa	437
Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu	
100 105 110	
sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc	485
Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr	
115 120 125 130	
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc	527
Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala	
135 140	
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccttgctccc tgggaggcca	587
ggagcaagcg ccagagcaca agcaggagca aggagtggag cacaggcagg agccgacaca	647
agaacacaag caggaagagg ggcagaaaca ggaagagcaa gaagaggaac aggaagagga	707
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gacagactca gagcccaagt ttcactctga atctctatct tctaaccctt cctcttttgc	827
tccccgggta cganaagtag agtctactcc tatgataatg gagaacatcc aggagctcat	887
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<222> 147..374

<223> Von Heijne matrix

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<221> misc_feature

<222> 547

<223> n=a, g, c or t

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agcggcaaga tcgcatctcc cggctc atg ggc gac tat ctg ctg cgc ggt tac	173
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Met Gly Asp Tyr Leu Leu Arg Gly Tyr

-75

-70

cgc atg ctg ggc gag acg tgt gcg gac tgc ggg acg atc ctc ctc caa	221
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Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln

-65

-60

-55

gac aaa cag cgg aaa atc tac tgc gtg gct tgt cag gaa ctc gac tca	269
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Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser

-50	-45	-40	
gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc	317		
Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser			
-35	-30	-25	-20
caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc	365		
Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly			
-15	-10	-5	
tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag	413		
Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu			
1	5	10	
gga gct gca gca gga ctc aag gca gcc cag ggg cca cct gct cct gct	461		
Gly Ala Ala Ala Gly Leu Lys Ala Ala Gln Gly Pro Pro Ala Pro Ala			
15	20	25	
gtg cct cca aat aca rat gtc atg gcc tgc aca cag aca gcc ctc ttg	509		
Val Pro Pro Asn Thr Xaa Val Met Ala Cys Thr Gln Thr Ala Leu Leu			
30	35	40	45
caa aag ctg acc tgg gcc tct gct gaa ctg ggc tct anc acc tcc cyg	557		
Gln Lys Leu Thr Trp Ala Ser Ala Glu Leu Gly Ser Xaa Thr Ser Xaa			
50	55	60	
gga aaa mta gca tcc agc tgt gtg gcc tta tcc gcg cat gtg cgg agg	605		
Gly Lys Xaa Ala Ser Ser Cys Val Ala Leu Ser Ala His Val Arg Arg			
65	70	75	
ccc tgc gca gcc tgc agc agc tac agc act aag aga agc ccc	647		
Pro Cys Ala Ala Cys Ser Ser Tyr Ser Thr Lys Arg Ser Pro			
80	85	90	
tgagaaaaac ctctagaaaa acaaaaaaaaaa aaaaccc	684		

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tggaataagaa gtccactcac agaaatcctg aagatgccag ggctggcaaa tatgaaggta	180
aacacaaacg aaagaaaaga agaaagcaaa accaaaacca gcaccgatcc cgacatagat	240
cagtgacgtc tttttcttca g atg atc cta tgt ttc ctt ctt cct cat cat	291

	Met	Ile	Leu	Cys	Phe	Leu	Leu	Pro	His	His	
	-15					-10					
cgt ctt cag gaa gcc aga cag att caa gta ttg aag atg ctt cca agg											339
Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro Arg											
-5	1			5				10			
gaa aaa tta aga aga aga gaa gag aga aaa caa ata aat ggg aaa aaa											387
Glu Lys Leu Arg Arg Arg Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys											
	15		20			25					
raa agg aca aaa tat gaa aca cca aga aaa rga raa gga aaa aaa gga											435
Xaa Arg Thr Lys Tyr Glu Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly											
	30		35			40					
gga aac mac cmc wtw tkt cmc ctt tcc aar agg gac tgaaactggg											481
Gly Asn Xaa Xaa Xaa Xaa Xaa Leu Ser Lys Arg Asp											
	45		50			55					
ctgacccttt tgatttccaa vctcascgtt ttggtgtaag gcggccaaar aaggatgcgg											541
ascccagcac tgtgaagcct acaaaaacat tgatgcgctg gcttggggat ttgaatttga											601
acatctttca cactaagttc agactcatga aaccaatctt cagatgctct gtaaaccaca											661
taataaagag ttgggaaatt aaaaaaaaaa aa											693

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 <222> 74..1216

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 <222> 74..172
 <223> Von Heijne matrix
 score 5.80000019073486
 seq XLCLGMALCPRQA/TR

<220>
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 <222> 1627..1632

<220>
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 <222> 1640..1652

<400> 307												
atctcttggc gtctcaacgt tcggatcagc agcttttttc cattctctct ctccacttct												60
tcagtgaagca gcc atg agt tgg act gtg cct gtt gtg cgg gcc agc cag												109
	Met	Ser	Trp	Thr	Val	Pro	Val	Val	Arg	Ala	Ser	Gln
	-30								-25			
aga gtg agc tcg gtg gga gcg aat ktc cta tgc ctg ggg atg gcc ctg												157
Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu												
	-20			-15				-10				
tgt ccg cgt caa gca acg cgc atc ccg ctc aac ggc acc tgg ctc ttc												205
Cys Pro Arg Gln Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe												
	-5		1			5			10			
acc ccc gtg agc aag atg gcg act gtg aar agt gag ctt att gag cgt												253
Thr Pro Val Ser Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg												
	15			20					25			

ttc act tcc gar aag ccc gtt cat cac agt aag gtc tcc atc ata gga	301
Phe Thr Ser Glu Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly	
30 35 40	
act gga tcg gtg ggc atg gcc tgc gct atc agc atc tta tta aaa ggc	349
Thr Gly Ser Val Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly	
45 50 55	
ttg agt gat gaa ctt gcc ctt gtg gat ctt gat gaa rac aaa ctg aag	397
Leu Ser Asp Glu Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys	
60 65 70 75	
ggg gag acr atg gat ctt caa cat ggc agc cct ttc acg aaa atg cca	445
Gly Glu Thr Met Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro	
80 85 90	
aat att gtt tgt agc aaa rat tac ttt gtc aca gca aac tcc aac cta	493
Asn Ile Val Cys Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu	
95 100 105	
gtg att atc aca gca ggt gca cgc caa raa aag gga gaa acg cgc ctt	541
Val Ile Ile Thr Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu	
110 115 120	
aat tta stc cag cga aat gtg gcc atc ttc aag tta atg att tcc agt	589
Asn Leu Xaa Gln Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser	
125 130 135	
att gtc cag tac agc ccc cac tgc aaa ctg att att gtt tcc aat cca	637
Ile Val Gln Tyr Ser Pro His Cys Lys Leu Ile Val Ser Asn Pro	
140 145 150 155	
gtg gat atc tta act tat gta gct tgg aag ttg agt gca ttt ccc aaa	685
Val Asp Ile Leu Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys	
160 165 170	
aac cgt att att gga agc ggc tgt aat ctg ata mhg gct cgt ttt cgt	733
Asn Arg Ile Ile Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg	
175 180 185	
ttc ttg att gga caa aag ctt ggt atc cat tct gaa agc tgc cat gga	781
Phe Leu Ile Gly Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly	
190 195 200	
tgg atc ctc gga gag cat gga gac tca agt gtt cct gtg tgg agt gga	829
Trp Ile Leu Gly Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly	
205 210 215	
gtg aac ata gct ggt gtc cct ttg aag gat ctg aac tct gat ata gga	877
Val Asn Ile Ala Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly	
220 225 230 235	
act gat aaa gat cct gag caa tgg aaa aat gtc cac aaa gaa gtg act	925
Thr Asp Lys Asp Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr	
240 245 250	
gca act gcc tat gag att att aaa atg aaa ggt tat act tct tgg gcc	973
Ala Thr Ala Tyr Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala	
255 260 265	
att ggc cta tct gtg gcc gat tta aca gaa agt att ttg aag aat ctt	1021
Ile Gly Leu Ser Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu	
270 275 280	
agg aga ata cat cca gtt tcc acc ata act aag ggc ctc tat gga ata	1069
Arg Arg Ile His Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile	
285 290 295	
rat gaa gaa gta ttc ctc agt att cct tgt atc ctg gga gag aac ggt	1117
Xaa Glu Glu Val Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly	
300 305 310 315	
att acc aac ctt ata aag ata aag ctg acc cct gaa gaa gag gcc cat	1165
Ile Thr Asn Leu Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His	
320 325 330	

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ctg aaa aaa agt gca aaa aca ctc tgg gaa att cag aat aag ctt aag      1213
Leu Lys Lys Ser Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys
      335                      340                      345
ctt taaagttgcc taaaactacc attccgaaat tattgaagag atcatagata      1266
Leu
caggattata taacgaaatt ttgaataaac ttgaattcct aaaagatgga aacaggaaag      1326
taggtagagt gattttccta tttatttagt cctccagctc ttttattgag catccacgtg      1386
ctggacgata cttattttaca attcckaagt attttttggt cctctgatgt agcagcactt      1446
gccatgttat atatatgtag ttgrmatttg gttcccaaaa agtaggatgt aggtattttat      1506
tgtgttctag aaattccgac tcttttcatt agatatatgc tatttccttc attccttgcg      1566
gtttatacct atgttcattt atatgctgta aaaaagtagt agcttcttct acaatgtaaa      1626
aataaatgta catacaaaaa aaaaaamcmc                                1656

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<213> Homo sapiens

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<222> 48..164

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<222> 48..89
<223> Von Heijne matrix
      score 4
      seq YYMVCLFFRLIFS/EH

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<222> 482..487

<220>
<221> polyA_site
<222> 505..517

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aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac      56
                                   Met Tyr Tyr
atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att      104
Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile
      -10                      -5                      1                      5
ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca      152
Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro
                        10                      15                      20
aca tct gct ggc taaataaaga catgatcttc accttttggg attgttaatt      204
Thr Ser Ala Gly
      25
taaaatgggt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctgggtg      264
atztatatgg ctcttcacaa ggtgttattt tggggtatca aggtatggat gcttaaataca      324
gctgcaggaa gtaagaaaga agaaaaaagg agtgataaag ataaaaaaaa atcaaccttg      384
gtccttcac caaaacccat taatttccat atcatcatct gcataararg gaaaattcct      444
acwtgaccag gttactgcaa ggatktkaat tttgaatatt aaaatattat mcmcaattgg      504
aaaaaaaaaa aaa                                                  517

<210> 309

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<211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..334

<220>
 <221> sig_peptide
 <222> 185..295
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSYASSALSPCLT/AP

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 <221> polyA_signal
 <222> 355..360

<220>
 <221> polyA_site
 <222> 392..405

<400> 309
 atcaccttct tctccatcct tstctgggcc agtccccarc ccagtccttc tcttgacctg 60
 cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggctacct 120
 ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180
 tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
 -35 -30 -25
 aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
 Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
 -20 -15 -10
 ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg 325
 Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met
 -5 1 5 10
 cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc 374
 Pro Asp Asn
 tccaraaggg tttctaataaa caaaaaaaaaa a 405

<210> 310
 <211> 1087
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 195..347

<220>
 <221> sig_peptide
 <222> 195..272
 <223> Von Heijne matrix
 score 7.099999990463257
 seq LASLQWSLTLAWC/GS

<220>

<221> polyA_signal

<222> 1037..1042

<220>

<221> polyA_site

<222> 1071..1082

<400> 310

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aaagtgtaga acacggacct ctgagttatg ctcttgagag gtgccaaagc tgggctgttt      60
acctacctta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg      120
gaattttatc tagaaaagaa gactaagcag cttttgttct tctgtgacct agttgctggc      180
ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg      230
                Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg
                -25                -20                -15
cct ctc gct tct ttg cag tgg agc ctg aca ctg gcg tgg tgt ggc tcc      278
Pro Leu Ala Ser Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser
                -10                -5                1
ggc agc cac tgg aca gag aga cca akt cag akt tca ccg tgg akt tct      326
Gly Ser His Trp Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser
                5                10                15
ctg tca gcg acc acc agg ggg tgatcacacg gaaggtgaac atccaggtcg      377
Leu Ser Ala Thr Thr Arg Gly
                20                25
gggatgtgaa tgacaacgcg cccacatttc acaatcagcc ctacagcgtc cgcattccctg      437
araatacacc agtggggacg cccatcttca tcgtgaatgc cacagacccc gacttggggg      497
cagggggcag cgtcctctac tccttcacgc cccctccca attcttcgcc attgacagcg      557
ccgcgggtat cktcacagtg atccgggagc tggactacga taccacrcmg gcctaccagc      617
tcwcggtcwa cgccacagat caagacaara ccaggcctct gtccaccstg gccaaacttg      677
ccatcatcat cacagatgtc caggacatgg accccatctt catcaacctg ccttacagca      737
ccaacatcta cgagcattct cctccgggca cgacgggtgcg catcatcacc gccatagacc      797
aggataaagg acgtccccgg ggcattggct acaccatcgt ttcagggcat ctgtgtttac      857
aagaacccaa gatctctcag gagctcagga aaaggggctt gctgtgaggc tcagggttcc      917
catggacatt ctgagctgac cctcctcagc attggatctc ctggctcagg aactaggaac      977
gaagcttga tgttttctcc tttcctacag catctgtatt catttctat agttgccata     1037
ataaaatgcc actaacttag tggcttaaaa accaaaaaaa aaaaaccctt     1087
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<210> 311

<211> 916

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 90..815

<220>

<221> sig_peptide

<222> 90..179

<223> Von Heijne matrix
score 13.1999998092651
seq LLLLSTLVIPSAA/AP

<220>

<221> polyA_signal

<222> 883..888

<220>

<221> polyA_site

<222> 905..916

<220>

<221> misc_feature

<222> 487,661

<223> n=a, g, c or t

<400> 311

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aaaacagtac gtgggcggcc ggaatccggg agtccgggtga cccgggctgt ggtctagcat      60
aaaggcggag ccagaagaag gggcgggggt atg gga gaa gcc tcc cca cct gcc      113
                               Met Gly Glu Ala Ser Pro Pro Ala
                               -30                               -25

ccc gca agg cgg cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg      161
Pro Ala Arg Arg His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu
                               -20                               -15                               -10

gtg atc ccc tcc gct gca gct cct atc cat gat gct gac gcc caa gag      209
Val Ile Pro Ser Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu
                               -5                               1                               5                               10

agc tcc ttg ggt ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc      257
Ser Ser Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser
                               15                               20                               25

cga ctt ttc ctg aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc      305
Arg Leu Phe Leu Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe
                               30                               35                               40

tct gcc ccc atg gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag      353
Ser Ala Pro Met Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu
                               45                               50                               55

gag aac cag gag cac cag ctg ggg aac aac acc ctc tcc agc cac ctc      401
Glu Asn Gln Glu His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu
                               60                               65                               70

cag atc gac aag atg acc gac aac aag aca gga gag gtg ctg atc tcc      449
Gln Ile Asp Lys Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser
75                               80                               85                               90

gag aat gtg gtg gca tcc att caa cca vcg gag ggg anc ttc gag ggt      497
Glu Asn Val Val Ala Ser Ile Gln Pro Xaa Glu Gly Xaa Phe Glu Gly
95                               100                               105

gat ttg aag gth ccc agg atg gag gar aag gag gcc ctg gta ccc mtc      545
Asp Leu Lys Val Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Xaa
110                               115                               120

car aag gcc acg gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc      593
Gln Lys Ala Thr Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala
125                               130                               135

ttc tgg atc att aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg      641
Phe Trp Ile Ile Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu
140                               145                               150

gag ggc ggc cac tgg ctc anc gar aag cga cac cgc ctg cag gcc atc      689
Glu Gly Gly His Trp Leu Xaa Glu Lys Arg His Arg Leu Gln Ala Ile
155                               160                               165                               170

cgg gat gga ctc cgc aag ggg acc cac aag gac rtc cta daa rag ggg      737
Arg Asp Gly Leu Arg Lys Gly Thr His Lys Asp Xaa Leu Xaa Xaa Gly
175                               180                               185

acc gar agc tcc tcc cac tcc agg ctg tcc ccc cga aar amm cac tta      785
Thr Glu Ser Ser Ser His Ser Arg Leu Ser Pro Arg Lys Xaa His Leu
190                               195                               200

ctg tac atc ctc arg ccc tct cgg cag ctg targgggtggg gaccggggar      835
Leu Tyr Ile Leu Xaa Pro Ser Arg Gln Leu
```

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      205              210
macctgcctg tagcccccac caraccctgc cccaagcacc atatggaaat aaagttcttt      895
cttacatcca aaaaaaaaaa a                                     916

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<211> 583
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..513

<220>
<221> sig_peptide
<222> 52..231
<223> Von Heijne matrix
      score 4
      seq LVRRTLLVAALRA/WM

<220>
<221> polyA_signal
<222> 553..558

<220>
<221> polyA_site
<222> 572..583

<400> 312
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                                         Met Gly
                                         -60
agt aaa tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag      105
Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln
      -55              -50              -45
agg cgg cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg      153
Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val
      -40              -35              -30
aar gca gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc      201
Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg
      -25              -20              -15
agg acc ctg ctg gtt gct gcc ctg agg gcc tgg atg att cag tgc tgg      249
Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp
      -10              -5              1              5
tgg agg acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg      297
Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu
      10              15              20
ttr ggg gtc tac gtc atc cag gag cag gcg gcg gtc aag ctg cag tcc      345
Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu Gln Ser
      25              30              35
tgc atc cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat      393
Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn
      40              45              50
gct ctg tgc ttg ttc cag gtc cca aaa agc agc ctt gcc ttc caa act      441
Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe Gln Thr
      55              60              65              70
gat ggc ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag      489

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Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu	
75 80 85	
ttc cac att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg	543
Phe His Ile Glu Ile Leu Ser Ile	
90	
cactacccta ataaatgtct gaccaggtaa aaaaaaaaaa	583
<210> 313	
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<212> DNA	
<213> Homo sapiens	
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<221> CDS	
<222> 172..438	
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<221> sig_peptide	
<222> 172..354	
<223> Von Heijne matrix	
score 4.69999980926514	
seq LLPCNLHCSWLHS/SP	
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<222> 682..687	
<220>	
<221> polyA_site	
<222> 685..697	
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cagagccatc ggccaggtac caaagctcag ctgtatggat tcccaacagg aggacctgcg	120
cttccctggg acccattgtt gtactggatt aacaagcgac ggcgctacgg c atg aat	177
Met Asn	
-60	
gca gcc atc aac acg ggc cct gcc cct gct gtc acc aag act gag act	225
Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr Glu Thr	
-55 -50 -45	
gag gtc cag aat cca gat gtt ctg tgg gat ttg gac atc ccc gaa gcc	273
Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro Glu Ala	
-40 -35 -30	
agg agc cat gct gac caa gac agc aac ccc aag gcg gaa gcc ctg ctc	321
Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala Leu Leu	
-25 -20 -15	
ccc tgc aac ctg cac tgc agc tgg ctc cac agc agc ccc agg cca gat	369
Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg Pro Asp	
-10 -5 1 5	
ccc cat tcc cac ttc cca tct ktc agg agg tgc cct ttg ccc cac cct	417
Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro His Pro	
10 15 20	
tgt gca acc tac ccc ccs kgc tgaaccactc tgtctcctat cctttggcca	468
Cys Ala Thr Tyr Pro Pro Xaa	
25	
cctgtcctga aaggaatggt ctcttccatt cctcctcgaa tctggcccag gaagaccata	528
gcttcaatqy caagcctttt ccttcaaaac tqtagcctcc tctcactgaa ggtgggagct	588

gcaggaatca ggtgcagagt aggaaatgga actaacctca ggaaggtggt attgacagag 648
gtcaggaccc acctggatgt catgctatga aacattaaaa gaaaaaaaaa 697

<210> 314
<211> 803
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..366

<220>
<221> sig_peptide
<222> 148..225
<223> Von Heijne matrix
score 5.5
seq LFTLLFLIMLVLK/LD

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<221> polyA_signal
<222> 770..775

<220>
<221> polyA_site
<222> 792..803

<400> 314
aaatggggggg aaaagggcgg aaaaggacaa ggatccaaac tggcgaattht gctgatcttc 60
gcgtccctct ccgctttccg gccggcagcg ctgccagggt atatttcctt tttcccgatc 120
ctgcaacagc ctctttaaac tgttttaa atg aga atg tcc ttg gct cag aga gta 174
Met Arg Met Ser Leu Ala Gln Arg Val
-25 -20
cta ctc acc tgg ctt ttc aca cta ctc ttc ttg atc atg ttg gtg ttg 222
Leu Leu Thr Trp Leu Phe Thr Leu Leu Phe Leu Ile Met Leu Val Leu
-15 -10 -5
aaa ctg gat gag aaa gca cct tgg aac tgg ttc ctc ata ttc att cca 270
Lys Leu Asp Glu Lys Ala Pro Trp Asn Trp Phe Leu Ile Phe Ile Pro
1 5 10 15
gtc tgg ata ttt gat act atc ctt ctt gtc ctg ctg att gtg aaa atg 318
Val Trp Ile Phe Asp Thr Ile Leu Leu Val Leu Leu Ile Val Lys Met
20 25 30
gct ggg cgg tgt aag tct ggc ttt gac ctc gac atg gat cac aca ata 366
Ala Gly Arg Cys Lys Ser Gly Phe Asp Leu Asp Met Asp His Thr Ile
35 40 45
taaaaaaaaa aacctggtac ctcatctcac tgtkacttaa attasccttc tgcctcgcac 426
tctgtgctaa actggaacag tttactacca tgaatctatc ctatgtcttc attcctttat 486
gggccttgct ggctggggct ttaacagaac tcggatataa tgtctttttt gtgaaagact 546
gacttctaag tacatcatct cctttctatt gctgttcaac aagttaccat taaagtgttc 606
tgaatctgtc aagcttcaag aataccagag aactgagggg aaataccaaa tgtagtttta 666
tactacttcc ataaaacagg attggtgaat cacggacttc tagtcaacct acagcttaat 726
tattcagcat ttgagttatt gaaatcctta ttatctctat gtaaataaag tttgttttgg 786
acctcaaaaa aaaaaaa 803

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<213> Homo sapiens

<220>

<221> CDS

<222> 175..336

<220>

<221> sig_peptide

<222> 175..276

<223> Von Heijne matrix

score 3.70000004768372

seq SVLNVGHLLFSSA/CS

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<222> 812..823

<400> 315

aaggcgcgcg	cgaccggcgg	ctctttggcg	cggattaggg	ggtctcggcg	agggagtc	cat	60
caagctttgg	tgtatgtgtt	ggccggttct	gaagtcctga	agaagctctg	ctgaggaaga		120
ccaaagcagc	actcgttgcc	aattagggaa	tggaccgttt	gggttccttt	agca atg		177
					Met		
atc cct ctg ata agc cac ctt gcc gag gct gct cct cct acc tca tgg							225
Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser Trp							
	-30		-25		-20		
agc ctt ata tca agt gtg ctg aat gtg ggc cac ctg ctt ttt tcc tct							273
Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser Ser							
	-15		-10		-5		
gct tgc agt gtt tca ctg gag gct ttg agt aca aga aac atc aaa gcg							321
Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys Ala							
1	5		10		15		
atc ata ctt atg aaa taatggcttc agattttcct gtccttgatc ccagctggac							376
Ile Ile Leu Met Lys							
	20						
tgctcaagaa	raaatggccc	ttttagaasc	tgtgatggac	tgtggctttg	gaaattggca		436
ggatgtagcc	aatcaaagt	gcaccaarac	caaggaggag	tgtgagaagc	actatatgaa		496
gcatttcac	aataaccyc	tgtttgcatc	trscctgctg	aacctgaaac	aascagrnga		556
agcaaaaact	gctgacacag	ccattccatt	tcactctaca	ratgaccctc	cccgaccac		616
ctttgactcc	ttgctttctc	gggacatggc	cgggtacwtg	ccmgctcgag	cagatttcac		676
tgaggaattt	gacaattatg	cagaatggga	cttgagagac	attgattttg	ttgaagatga		736
ctcggaacatt	ttacatgctc	tgaagatggc	tgtggtagat	atctatcatt	ccaggttaaa		796
ggagagacaa	agacgaaaaa	aaaaaaaa					823

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<211> 823

<212> DNA

<213> Homo sapiens

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<222> 191..553

<220>

<221> sig_peptide

<222> 191..304

<223> Von Heijne matrix

score 5.69999980926514

seq LAFLSCLAFLVLD/TQ

<220>

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<222> 766..771

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<221> polyA_site

<222> 804..817

<220>

<221> misc_feature

<222> 819

<223> n=a, g, c or t

<400> 316

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gtggagatgt gctgaggtct tctccctgat cgtcttctcc tccctgctga ccgacggcta      180
ccagaackag atg gag tct ccg cag ctc cac tgc att ctc aac agc aac      229
          Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn
                    -35                                -30
agc gtg gcc tgc agc ttt gcc gtg gga gcc ggc ttc ctg gcc ttc ctc      277
Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
-25                                -20                                -15                                -10
agc tgc ctg gcc ttc ctc gtc ctg gac aca cag gag acc cgc att gcc      325
Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
                    -5                                1                                5
ggc acc cgc ttc aag aca gcc ttc cag ctc ctg gac ttc atc ctg gct      373
Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala
                    10                                15                                20
gtt ctc tgg gca gtt gtc tgg ttc atg ggt ttc tgc ttc ctg gcc aac      421
Val Leu Trp Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn
                    25                                30                                35
caa tgg cag cat tcg ccg ccc aaa gar kkc ctc ctg ggg agc agc agt      469
Gln Trp Gln His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser
40                                45                                50                                55
gcc cag gca gcc atc ggc stt cac ctt ctt ctc cat cct tgt ctg gat      517
Ala Gln Ala Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp
                    60                                65                                70
att cca rgc cta cct ggc akk cca gga cct ccg aaa tgatgctcca      563
Ile Pro Xaa Leu Pro Gly Xaa Pro Gly Pro Pro Lys
                    75                                80
gtcccttacm arcgcttctt ggatgaaggt ggcctgggtgs kkaacaccct ccccttgccc      623
tctgccaaaca gcctgtgaac atgcccacca ctggcccca cagcctgagt tatgctagct      683
ctgccctgtc cccctgtctg accgctcmaa agtccccccg gcttgctatg atgcctgaca      743
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aacaacaaaaaaa aaaahncctt      823

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<210> 317

<211> 1112

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<221> CDS

<222> 106..603

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<222> 106..216
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<222> 1102..1112

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tcgggtcctg agaccaggtc ctcagccagc agagccacgt tcctt atg agc acc gtg      117
                                     Met Ser Thr Val
                                     -35
ggt tta ttt cat ttt cct aca cca ctg acc cga ata tgc ccg gcg cca      165
Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile Cys Pro Ala Pro
      -30      -25      -20
tgg gga ctc cgg ctt tgg gag aag ctg acg ttg tta tcc cca gga ata      213
Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu Ser Pro Gly Ile
      -15      -10      -5
gct gtc act ccg gtc cag atg gca ggc aag aag gac tac cct gca ctg      261
Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp Tyr Pro Ala Leu
      1      5      10      15
ctt tcc ttg gat gag aat gaa ctc gaa gag cag ttt gtg aaa gga cac      309
Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe Val Lys Gly His
      20      25      30
ggt cca ggg ggc cag gca acc aac aaa acc agc aac tgc gtg gtg ctg      357
Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn Cys Val Val Leu
      35      40      45
aar mac atc ccc tca ggc atc gtt gta aag tgc cat cag aca aga tca      405
Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His Gln Thr Arg Ser
      50      55      60
gtt gat cag aac aga aag cta gct cgg aaa atc cta caa gag aaa gta      453
Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu Gln Glu Lys Val
      65      70      75
rat gtt ttc tac aat ggt gaa aac agt cct gtt cac aaa gaa aaa cga      501
Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His Lys Glu Lys Arg
      80      85      90      95
gaa gcg gcg aag aaa aaa car gaa agg aaa aaa aga gca aag gaa acc      549
Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg Ala Lys Glu Thr
      100      105      110
ctg gaa aaa aag aas ctm ctt aaa raa ctg tgg gag tca agt aaa aag      597
Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu Ser Ser Lys Lys
      115      120      125
gtc cac tgagaaaaga attagagatt ccaactgaca gaatctgcc aagctccca      653
Val His
gggaataatg gtggcgagtt ccatcaccag cattattata gtgcttcaaa agaaatattt      713
ttgatgaact taaaagacaa caaatattt taaatggtgc actaaactgt agtgaacaga      773
gacatgcacg attcaagaat aaaactcggc cgggcacggt ggacggtgcc tcacatctgt      833
aatcccagca ctttgggagg ccgagggcggg cggatcactt gaggtcagga gtttgagacc      893
agcctggcca acatggtgaa acccgtctc tactaaaaat acaaaaaatt agccaggcat      953
ggtggcgggc acctgtaatc ccagctactc gggaggccga ggcaggagaa ttgctgaac      1013
ctgggaggcg gaggttgag tgagctgaga tcgcgccact gcactcaagc ctgggcaaca      1073
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<210> 318
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 <223> Von Heijne matrix
 score 6.30000019073486
 seq GVGLVTLLGLAVG/SY

<220>
 <221> polyA_signal
 <222> 1583..1588

<220>
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 <222> 1614..1623

<220>
 <221> misc_feature
 <222> 1597
 <223> n=a, g, c or t

<400> 318
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 Met Gly Ile
 -25
 cag acg agc ccc gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act 103
 Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr
 -20 -15 -10
 ctg ctg ggc ctg gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg 151
 Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg
 -5 1 5
 cct cag gtc act ctg ctg gac ccc aat gaa aag tac ctg cta cga ctg 199
 Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu
 10 15 20 25
 cta gac aag acg act gtg agc cac aac acc aag agg ttc cgc ttt gcc 247
 Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala
 30 35 40
 ctg ccc acc gcc cac cac act ctg ggg ctg cct gtg ggc aaa cat atc 295
 Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly Lys His Ile
 45 50 55
 tac ctg tcc acm mga att gat ggc agc ctg gtc atc agg cca tac act 343
 Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr
 60 65 70
 cct gtc acc agt gat gag gat caa ggc tat gtg gat ctt gtc mtc aag 391
 Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Xaa Lys
 75 80 85
 gtc tac ctg aag ggt gtg cac ccc aaa ttt cct gag gga ggg aar atg 439
 Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met

90	95	100	105	
tct cak tac ctg gat asc ctg aaa gtt ggg gat btg gtg gaa ttt csg				487
Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val Glu Phe Xaa				
	110	115	120	
ggg cca agc ggg ttg ctc act tac act gga aaa ggg cat ttt aac att				535
Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile				
	125	130	135	
cag ccc aac aag aat ctc cac cag aac ccc gag tgg cga aga aac tgg				583
Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg Arg Asn Trp				
	140	145	150	
gaa tgattgccgg cgggacagga atcaccccaa tgctacagct gatccggggcc				636
Glu				
atcctgaaag tccctgaaga tccaacccag tgctttctgc tttttgccaa ccagacagaa				696
aaggatatca tcttgcgga ggacttagag gaactgcagg cccgctatcc caatcgcttt				756
aagctctggt tcaactctgga tcatcccca aaagrttggg cctacagcaa gggctttgtg				816
actgccgacw tgatccggga acacctgccc gctccagggg atgatgtgct ggtactgctt				876
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tcacaaaaga tgcgattcac ctactgagca tctccagct tccctggtgc tgttcgctgc				996
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ggttttttca gttrsatcka gagctgaaat ctggatagta cctgcaggaa caatattcct				1116
gtagccatgg aagagggcca aggcctcagtc actccttgga tggcctccta aatctccccg				1176
tggcaacagg tccaggagag gcccatggag cagtctcttc catggagtaa gaaggaaggg				1236
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ttgtgtctgt gatgaaagga acagtctgtg caatgggttt tacttaaact tcaactgttca				1356
acctatgagc aaatctgtat gtgtgagtat aagttgagca tagcatactt ccagaggtgg				1416
tcttatggag atggcaagaa aggaggaaat gatttcttca gatctcaaag gagtctgaaa				1476
tatcatattt ctgtgtgtgt cdctctcagc ccctgcccad gctagaggga wacagctact				1536
gataatcgaa aactgctgtt tgtgggcarg aaccctggc tgtgcaaata atggggctga				1596
ngccctgtgt gatattgaaa aaaaaaa				1623

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 <222> 99..371

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 <222> 99..290
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LFIVVCVICVTLN/FP

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 <222> 513..524

<400> 319
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Met Thr Pro Arg Ile Leu
-60
agc gaa gtc cag ttt tca gca ttt tgt cct tat tgg aca ata gca agg      164
Ser Glu Val Gln Phe Ser Ala Phe Cys Pro Tyr Trp Thr Ile Ala Arg
-55 -50 -45
ata tta gaa cgt gtt ggt tcc gcg tgc ttc cgt ctt gag tta tgt gct      212
Ile Leu Glu Arg Val Gly Ser Ala Cys Phe Arg Leu Glu Leu Cys Ala
-40 -35 -30
gct att gtc gga tat ttt gtc tta gat gta cgt act ttc ctg ttc att      260
Ala Ile Val Gly Tyr Phe Val Leu Asp Val Arg Thr Phe Leu Phe Ile
-25 -20 -15
gtg gta tgt gta att tgc gtt act ttg aat ttt cca cgt ttt tac ttt      308
Val Val Cys Val Ile Cys Val Thr Leu Asn Phe Pro Arg Phe Tyr Phe
-10 -5 1 5
ctt tgt ctc tca tca ctt acc gct ttt ggg acc ccc ccc atc ggg gtt      356
Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly Thr Pro Pro Ile Gly Val
10 15 20
cac att ccc tct ccc tararcacac tcccttggat ttcctcradt ggggtctgct      411
His Ile Pro Ser Pro
25
gcggtgaagc tttcccatTTt tatgtgcaga ttatttttcag agggatatata gaattcaggc      471
agctgttttcg ttgtagcaca ttaaaaatat tttcccactt caaaaaaaaaa aaacc      526

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<220>
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<222> 978..989

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<222> 569
<223> n=a, g, c or t

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Met Arg Arg Ile
-20
tcc ctg act tct agc cct gtg cgc ctt ctt ttg tdt ctg ctg ttg cta      103
Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Xaa Leu Leu Leu Leu
-15 -10 -5
cta ata gcc ttg gag atc atg gtt ggt ggt cac tct ctt tgc ttc aac      151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn

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	1		5		10		
ttc act ata aaa tca ttg tcc aga cct gga cag ccc tgg tgt gaa gcg						199	
Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala							
15		20		25			
cat gtc ttc ttg aat aaa aat ctt ttc ctt cag tac aac agt gac aac						247	
His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn							
30	35	40	45				
aac atg gtc aaa cct ctg ggc ctc ctg ggg aag aag gta tat gcc acc						295	
Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr							
50	55	60					
agc act tgg gga gaa ttg acc caa acg ctg gga gaa gtg ggg cga gac						343	
Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu Val Gly Arg Asp							
65	70	75					
ctc agg atg ctc ctt tgt gac atc aaa ccc car ata aag acc agt gat						391	
Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile Lys Thr Ser Asp							
80	85	90					
cct tcc act ctg caa gtc kar atk ttt tgt caa cgt gaa gca gaa cgg						439	
Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg Glu Ala Glu Arg							
95	100	105					
tgc act ggt gca tcc tgg cag ttc gcc acc aat gga gag aaa tcc ctc						487	
Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly Glu Lys Ser Leu							
110	115	120	125				
ctc ttt gac gca atg aac atg acc tgg aca gta att aat cat gaa gcc						535	
Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile Asn His Glu Ala							
130	135	140					
agt wag atc aag gag aca tgg aag aaa gac aga ngg ctg gaa aak tat						583	
Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa Leu Glu Xaa Tyr							
145	150	155					
ttc agg aag ctc tca aar gga gac tgc gat cac tgg ctc agg gaa ttc						631	
Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp Leu Arg Glu Phe							
160	165	170					
tta ggg cac tgg gaa gca atg cca raa ccg ama gtg tcm cca rta aat						679	
Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val Ser Pro Xaa Asn							
175	180	185					
gct tca raw atc cac tgg tct tct tct art cta cca raw ara tgg atc						727	
Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro Xaa Xaa Trp Ile							
190	195	200	205				
atc ctg ggg gca ttc atc ctg tta vtt tta atg gga att gtt ctc atc						775	
Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly Ile Val Leu Ile							
210	215	220					
tgt gtc tgg tgg caa aat ggc ara ara tcc acc tad arg tgataccacg						824	
Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa Xaa							
225	230						
gcggcgcaaa attgttcacc tgttggtctc gatcgctgac agccttggtt cccactgctg						884	
tgtgttccct gagtcaagtg gaggcggagc ctgcaatgag cggaratcgc gcctctgcat						944	
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<220>
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 <222> 3..581

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<221> sig_peptide

<222> 3..182

<223> Von Heijne matrix

score 6.69999980926514

seq LWPFLTWINPALS/IC

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<221> polyA_site

<222> 1006..1016

<400> 321

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ccc tgc tca gga caa cag cag cct ttc ccg ttt gga gcc tca aac atc      95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile
-45                -40                -35                -30
cca cta ctc ctg ggc agg agc aga aag gtg gct cga ggt gca ccg gtc      143
Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val
                -25                -20                -15
ctg tgg cca ttt ctc act tgg ata aac cct gca ctg tcc atc tgt gac      191
Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp
                -10                -5                1
ccc tta gga tcc tgc gga tgg cyw tgc cac acg gcc car gtc cct gcg      239
Pro Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala
    5                10                15
ccc ctg car ttg cct act gcc tgt cct ccc ctc cca cat ggc acc cgg      287
Pro Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg
20                25                30                35
gct gta ggc ccc acg cca ggc ctc ctc cct gag gct gca gcc cca sgc      335
Ala Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa
                40                45                50
acg tgk ggg gca ctg tcc tca cgc agc agg cac tgg tca tgt tcc att      383
Thr Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile
                55                60                65
gtc arc tgc ctc cac ctg cac ara ctc ctg tct gtg gag acc aga arc      431
Val Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa
    70                75                80
ttc cas aaa cat ctg ttg gtg ctg ctg gtg gct gtg gcc cat agt gtt      479
Phe Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val
    85                90                95
ctg gaa cca cct gcc ctg gtc cca aat gtg cag tgt gag atg tgc aca      527
Leu Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr
100                105                110                115
cac tca ggg ccc cgt gac ctg gaa gcc gca gtc gtg tcc cca gca cct      575
His Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro
                120                125                130
tgg gaa tgagcctgtc ctctgtgtga aggaggggggt ggttctcaaa ccaactgactc      631
Trp Glu
ttggtgctca ggagggggcct gctgctgtcc tgggcatggg gtggtcattg ttcaagactg      691
aggcagactc agtcttttgaa aggggtgcaga ggccaggcgc ggtggctcac gcctgtaatt      751
ccagcacttt gggaggccaa ggtggacaga tcatgaggtc aggagttcga gaccagcctg      811
gccaatacgg tgaaaccgca tctctactaa rraatawcaw aaattagtcg ggcatgggtg      871
atgtgtgctt gtagtcccag ctactcatga ggyctgaggc agaagaatca cctgaatctg      931
ggaggcagag gttgcagtga accaagatcg cagcactgta caccagcctg ggcgacagag      991
tgagactccg tctcaaaaaa aaaaam                                     1017
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<210> 322
 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..427

<220>
 <221> sig_peptide
 <222> 107..190
 <223> Von Heijne matrix
 score 3.79999995231628
 seq RFLSLSAADGSDG/SH

<220>
 <221> polyA_signal
 <222> 499..504

<220>
 <221> polyA_site
 <222> 516..529

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<400> 322
aaagtcagcg ctggagtcgg ctaggcggct ggaaacggcg gctgccgcgc gtgactcagg      60
gaggcggggag gccgmssggmg gagctcttcc tgcaggcgtg garacc atg gtg ctc      115
                               Met Val Leu
acg ctc gga gaa agt tgg ccg gta ttg gtg ggg agg agg ttt ctc agt      163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
-25                -20                -15                -10
ctg tcc gca gcc gac ggc agc gat ggc agc cac gac agc tgg gac gtg      211
Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser Trp Asp Val
                -5                1                5
gag cgc gtc gcc gag tgg ccc tgg ctc tcc ggg acc att cga gct gtt      259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
                10                15                20
tcc cac acc gac gtt acc aag aag gat ctg aag gtg tgt gtg gaa ttt      307
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys Val Glu Phe
                25                30                35
gak ggg gaa tct tgg agg aaa aga aga tgg ata gaa gtc tac agc ctt      355
Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val Tyr Ser Leu
40                45                50                55
cta agg aaa gca ttt tta gta aaa cat aat ttg gtt tta gct gaa cga      403
Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu Ala Glu Arg
                60                65                70
aag tca cct gaa att tct tgg ggt taaccatctt tagttaaatg gaattttaat      457
Lys Ser Pro Glu Ile Ser Trp Gly
                75
ttaaatgacg ctttgctaatt ttttaagtgtt aagcattttg cattaaaata ttcataataat      517
aaaaaaaaaa aa      529
```

<210> 323
 <211> 1046
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..407

<220>
 <221> sig_peptide
 <222> 45..83
 <223> Von Heijne matrix
 score 5.69999980926514
 seq MLVLRSALETRALA/SR

<220>
 <221> polyA_signal
 <222> 1008..1013

<220>
 <221> polyA_site
 <222> 1032..1042

<400> 323
 aaaaggacac ggctggctgc ttttctcagc gccgaagccg cgcc atg ctc gtc ctc 56
 Met Leu Val Leu
 -10
 aga agc gcc ctg act cgg gcg ctg gcc tca cgg acg ctg gcg cct cag 104
 Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr Leu Ala Pro Gln
 -5 1 5
 atg tgc tca tct ttt gct acg gga ccc aga caa tac gat gga ata ttc 152
 Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr Asp Gly Ile Phe
 10 15 20
 tat gaa ttt cgt tct tat tac ctt aag ccc tca aag atg aat gag ttc 200
 Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys Met Asn Glu Phe
 25 30 35
 ctg gaa aat ttt gag aaa aac gct caa ctt cgg aca gct cac tct gaa 248
 Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr Ala His Ser Glu
 40 45 50 55
 ttg gtt gga tac tgg agt gta kaa ttt gga ggc aga atg awt aca gtg 296
 Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg Met Xaa Thr Val
 60 65 70
 ttt cat att tgg aag tat gat aat ttt gct cat cga act gaa ttt cag 344
 Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Glu Phe Gln
 75 80 85
 aaa gcc ttg gcc aaa gat aag gaa tgg caa gaa caa ttc ctc att cca 392
 Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Pro
 90 95 100
 aat ttg gct ctc aat tgataaaca gatagtgaga ttacttatct ggtacatgg 447
 Asn Leu Ala Leu Asn
 105
 tgcaaattag aaaaacctcc aaaagaagga gtctatgaac tggccacttt tcagatgaaa 507
 cctgggtgggc cagctctgtg ggggtgatgca tttaaaaggg cagttcatgc tcatgtcaat 567
 ctaggctaca caaaactagt tggagtgttc cacacagagt acggagcact caacagagtt 627
 catgttcttt ggtggaatga gagtgcagat agtcgtgcag ctgggagaca taagtcccat 687
 gaggatccca gagttgtggc agctgttcgg gaaagtgtca actacctagt atctcagcag 747
 aatatgcttc tgattcctac atcgttttca ccaactgaaat agttttctac tgaaatacaa 807
 aacatttcat taactgctat aggatctgtc tgctaattgt gcttaaattc tcccaagagg 867
 ttctcacttt tatttgaagg aggtggttaag ttaatttgct atgtttcttg cattatgaag 927
 gctacatctg tgctttgtaa gtaccacttc aaaaaatakt tctgtttact ttctgcatgg 987
 tatttcagtg tctgtcatac attaaaaata cttgtcactg tttyaaaaaa aaaaammcc 1046

<210> 324
 <211> 880
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 201..332

<220>
 <221> sig_peptide
 <222> 201..251
 <223> Von Heijne matrix
 score 7.80000019073486
 seq VLWLISFFTFTDG/HG

<220>
 <221> polyA_site
 <222> 869..880

<220>
 <221> misc_feature
 <222> 97,785,797,808
 <223> n=a, g, c or t

<400> 324
 aattgctgat ggatcagtga gcctgtgttc atgccagtga gctgctgtgg ctcagatact 60
 gatactttct ttccaaacag cataagaagt gattgancca caagtatact gaaggmargg 120
 yhcccwsvr tyctggwgtg amgagataaa tcaccagtca cagactatgc acccgactgc 180
 tgctgttcag tccagggaaa atg aaa gtt gga gtg ctg tgg ctc att tct ttc 233
 Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe
 -15 -10
 ttc acc ttc act gac ggc cac ggt ggc ttc ctg ggg gtg agt tgg tgc 281
 Phe Thr Phe Thr Asp Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys
 -5 1 5 10
 tat gtc tca tat ctc ttc tca act aac tct cct ctc tcg ttc cgg cgc 329
 Tyr Val Ser Tyr Leu Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg
 15 20 25
 att tagaaccct cactctctag gggactgcaa ctgcataatt taatgtactt 382
 Ile
 gagatcagaa gtccctgagtt ctcgtttcaa cattaccaac attcactgtg tggccttgga 442
 taagtragtc atttcatctc ttccggagctt agatgatcma actgcaarag gaggatcttt 502
 gattamacta tcttagagat cttttccagt tcaacacatg ctgtactatg gcttctcgga 562
 tgcagaaaaa tcacatggat ggacattagc aatccttara cactgtcttt cctgtctaca 622
 ctgccttgag tgatgckttc atctaggatc atgggtttta tattctctac atgctgatga 682
 ctcccagctg tatagctcca tctcagaacc tctcccctgt ccacactcac atatccatta 742
 cctacgtgtt atttccagct gggaaatcca gcggaacctc ggnaacttca tttgnttcaa 802
 aatcgnaacc caatccttct tgcctatctc agcaagtggg atcactatct ttccagctac 862
 ttaggcaaaa aaaaaaaaaa 880

<210> 325
 <211> 1217
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 217..543

<220>
 <221> sig_peptide
 <222> 217..255
 <223> Von Heijne matrix
 score 6.40000009536743
 seq MCLLTALVTQVIS/LR

<220>
 <221> polyA_site
 <222> 1206..1217

<220>
 <221> misc_feature
 <222> 307
 <223> n=a, g, c or t

<400> 325
 aatgccagtgc tcagcttctc tccgaaaact gggtaatacgc aaatgggtctt tattgggttgt 60
 gaacactcga gctgagaaac attttaggat ctttgtgtct tttgtgatga tttgtttct 120
 graagrwwga aasctgtcta aaaatattca agtgtgcaac caaggattta gatgaagcca 180
 gcaaacaaag gaatcatgta atcaggacct gagcga atg tgc tta ctc acg gcg 234
 Met Cys Leu Leu Thr Ala
 -10
 tta gtt aca cag gtg att tcc tta aga aaa aat gca gag aga act tgt 282
 Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
 -5 1 5
 tta tgc aag agg aga tgg ccc tgg ngc ccc tgc ccc cgg atc tac tgc 330
 Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
 10 15 20 25
 tca tcc acc cca tgc gat tcc aaa ttc ccc acc gtc tac tcc agt gcc 378
 Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser Ala
 30 35 40
 cca ttc cat gcc ccc ctc ccc gtc cag aat tcc tta tgg ggg cac ccg 426
 Pro Phe His Ala Pro Leu Pro Val Gln Asn Ser Leu Trp Gly His Pro
 45 50 55
 ctc cat ggt tgt tcc tgg caa tgc cac cat ccc cag gga car aat ctc 474
 Leu His Gly Cys Ser Trp Gln Cys His His Pro Gln Gly Gln Asn Leu
 60 65 70
 cag cct gcc agt ctc cad acc cat ctc tcc aag ccc aag cgc cat ttt 522
 Gln Pro Ala Ser Leu Xaa Thr His Leu Ser Lys Pro Lys Arg His Phe
 75 80 85
 ara aar aar rra tgt caa gcc tgatgaarac atgagtggca aaaacattgc 573
 Xaa Lys Lys Xaa Cys Gln Ala
 90 95
 aatgtacara aatgagggtt tctatgctga tccttacctt tatcacgagg gacggatgag 633
 catascctca tcccatggtg gacacccact ggatgtcccc gaccacatca ttgcatatca 693
 ccgcaccgcc atccggtcag cgagtgttta ttgtaacccc tcaatgcaag cggaaatgca 753
 tatggaacaa tcaactgtaca gacagaaatc aaggaaatat ccggaatgcc atttgccctac 813
 actgggctcc aaaacacccc ctgcctctcc tcacagakte agtgacctga ggatgataga 873
 catgcacgct cactataatg cccacggccc ccctcacacc atgcagccag accgggcctc 933
 tccgagccgc caggccttta aaaaggagcc aggcaccttg gtgtatatag aaaagccacg 993
 gagcgctgca ggattatcca gccttgtaga cctcggccct cctctaattg agaagcaagt 1053
 ttttgccctac agcacggcga caatacccaa agacagagag accagagaga ggatgcaagc 1113
 catggagaaa cagattgccca gtttaactgg ccttggttcag tctgcgcttt ttaaagggcc 1173

cattacaagt tatagcaaar atgCGTctag ctaaaaaaaaa aaaa

1217

<210> 326

<211> 959

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 18..446

<220>

<221> sig_peptide

<222> 18..140

<223> Von Heijne matrix
score 4.09999990463257
seq GILILWIIRLLFS/KT

<220>

<221> polyA_signal

<222> 930..935

<220>

<221> polyA_site

<222> 948..959

<400> 326

aaaggaagcg gctaact atg gcg acc gcc acg gag cag tgg gtt ctg gtg	50
Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val	
-40 -35	
gag atg gta cag gcg ctt tac gag gct cct gct tac cat ctt att ttg	98
Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu	
-30 -25 -20 -15	
gaa ggg att ctg atc ctc tgg ata atc aga ctt ctt ttc tct aag act	146
Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr	
-10 -5 1	
tac aaa tta caa gaa cga tct gat ctt aca gtc aag gaa aaa gaa gaa	194
Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu	
5 10 15	
ctg att gaa gag tgg caa cca gaa cct ctt gtt cct cct gtc cca aaa	242
Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys	
20 25 30	
gac cat cct gct ctc aac tac aac atc gtt tca ggc cct cca agc cac	290
Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His	
35 40 45 50	
aaa act gtg gtg aat gga aaa gaa tgt ata aac ttc gcc tca ttt aat	338
Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn	
55 60 65	
ttt ctt gga ttg ttg gat aac cct agg gtt aag gca gca gct tta gca	386
Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala	
70 75 80	
tct cta aag aag tat ggc gtg ggg act tgt gga ccc tgt gga ttt tat	434
Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr	
85 90 95	
ggc aca ttt gaa tgaaratgaa ggatcattga tttccttgtg tatggataat	486
Gly Thr Phe Glu	
100	

```

ccgggaacag gccaaactaaa tatttgatga atgtatgatt tcaaatacag tgaattccct 546
gggagtcac aaaraagacg gcattttatg gttgttttta ttaagtgtat attctttgct 606
cctgaaaatg ttattaaata attgttttagg ccgggcatgg tggctcatgc ctgtaatccc 666
agcactttca aaggctgagg caggcagatc acctgaggtc aggagttcaa aaccagcctg 726
gccaacatgc tgaaacctcg tctctactaa aaatacaaaa attagctggg cgtgggtggtg 786
grtgccctgtg gtcccagctr cgtgggagggc tgaggtggga gaattgcttc aacctgggag 846
gcggaggttg cagtgagccg agatcatgcc actgcactcc agcctgggca acagagcaag 906
actgtctcaa aaataaataa ataaataaaa ttgttttaat gaaaaaaaaa aaa 959

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<210> 327
<211> 921
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 29..724

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<220>
<221> sig_peptide
<222> 29..118
<223> Von Heijne matrix
      score 3.90000009536743
      seq VAHALSLPAESYG/NX

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<220>
<221> polyA_signal
<222> 886..891

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```

<220>
<221> polyA_site
<222> 910..920

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```

<220>
<221> misc_feature
<222> 301,319
<223> n=a, g, c or t

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<400> 327
aaggagccac gctttcgggg gttgcaag atg gcg gcc acc agt gga act gat 52
                               Met Ala Ala Thr Ser Gly Thr Asp
                               -30 -25
gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg ctt tct ctc 100
Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala Leu Ser Leu
      -20      -15      -10
cca gca gag tcg tat ggy aac grt yct gac att gag atg gct tgg gcc 148
Pro Ala Glu Ser Tyr Gly Asn Xaa Xaa Asp Ile Glu Met Ala Trp Ala
      -5      1      5      10
atg aga gca atg cag cat gct gaa gtc tat tac aag ctg att tca tca 196
Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu Ile Ser Ser
      15      20      25
gtt gac cca cag ttc ctg aaa ctc acc aaa gta gat gac caa att tac 244
Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp Gln Ile Tyr
      30      35      40
tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat gtg ttg grc 292
Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp Val Leu Xaa
      45      50      55

```

cca gaa gan ctc aag tca gaa tca gcn aaa gag ccc cca gga tac aat	340
Pro Glu Xaa Leu Lys Ser Glu Ser Ala Lys Glu Pro Pro Gly Tyr Asn	
60 65 70	
tct ttg cca ttg aaa ttg ctc gga acc ggg aag gct ata aca aag ctg	388
Ser Leu Pro Leu Lys Leu Leu Gly Thr Gly Lys Ala Ile Thr Lys Leu	
75 80 85 90	
ttt ata tca gtg ttc agg aca aag aag gag aga aag gag tca aca atg	436
Phe Ile Ser Val Phe Arg Thr Lys Lys Glu Arg Lys Glu Ser Thr Met	
95 100 105	
gag gag aaa aaa gag ctg aca gtg gag aag aag aga aca cca aga atg	484
Glu Glu Lys Lys Glu Leu Thr Val Glu Lys Lys Arg Thr Pro Arg Met	
110 115 120	
gag gag aga aag gag ctg ata gtg gag aag aaa aag agg aag gaa tca	532
Glu Glu Arg Lys Glu Leu Ile Val Glu Lys Lys Lys Arg Lys Glu Ser	
125 130 135	
aca gag aag aca aaa ctg aca aag gag gag aaa aag gga aag aag ctg	580
Thr Glu Lys Thr Lys Leu Thr Lys Glu Glu Lys Lys Gly Lys Lys Leu	
140 145 150	
aca aag aaa tca aca aaa gtg gtg aaa aag cta tgt aag gta tac agg	628
Thr Lys Lys Ser Thr Lys Val Val Lys Lys Leu Cys Lys Val Tyr Arg	
155 160 165 170	
gaa cag cac tct aga agc tat gac tca att gag act aca agt acc acg	676
Glu Gln His Ser Arg Ser Tyr Asp Ser Ile Glu Thr Thr Ser Thr Thr	
175 180 185	
gtg cta ctt gca cag acc cct ttg gtt aaa tgt aaa ttc ttg tac aat	724
Val Leu Leu Ala Gln Thr Pro Leu Val Lys Cys Lys Phe Leu Tyr Asn	
190 195 200	
tgaaggatac gcagaaggac atctttctag tctaacagtc aggagctgct ctgggtcattc	784
ccttgatatga actggtctaa agactgttag tggggtgtta gttgattttt cctgggtatac	844
tggtttcttg ctgacactac tgggtcaagta agaaatttgt aaataaattt cttttgggttc	904
ttattaamaa aaaaaaas	921

<210> 328
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 404..586

<220>
 <221> sig_peptide
 <222> 404..466
 <223> Von Heijne matrix
 score 4.09999990463257
 seq SLMFFSMMATCTS/NV

<220>
 <221> polyA_signal
 <222> 1304..1309

<220>
 <221> polyA_site
 <222> 1334..1344

<220>

<221> misc_feature
 <222> 211,213,232
 <223> n=a, g, c or t

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<400> 328
ataatttaaat gcaaaatata cttttatgaa tttcatgtta atattgtgaa atattaaaat    60
aattccacaa tagttgagaa aaatgagcat ttttttccat ttttaaaaaa tgcataaaaa    120
agacaattttt aaaatcctgg gamccawatt tatttagaag tagctgttag taaaacatta    180
gaaaaggagt caggccatba gggtatttat nbnaatctct aagcaattag gntgaagtta    240
ttaagtcaag cctagaaaag ctgcctcctt gtaaggcttt catgacaatg tatagtaatc    300
brcagtgtcc aattcttcgc actcctcagg aatatcacta cctcagggtta cggtagacag    360
gctataattg atgatgatgt tcagataact gaagacacaa taa atg aca ttc aga    415
                                   Met Thr Phe Arg
                                   -20
cat cag gac aat tcc ctc atg ttc ttt tct atg atg gcc acc tgt acc    463
His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met Ala Thr Cys Thr
      -15                                -10                                -5
agc aac gtg ggt ttc acc cac aca acg atg aac tgt tct ctt act tct    511
Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys Ser Leu Thr Ser
      1                                5                                10                                15
cca gtt gat ttt aaa gac ttg tta aga gtc tta cta ata aaa ttt ggg    559
Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu Ile Lys Phe Gly
      20                                25                                30
tat gat aga aaa tcc aca atc aaa tct tgaaccaa aacatattaa    606
Tyr Asp Arg Lys Ser Thr Ile Lys Ser
      35                                40
attactaata tttaagtgat ggaagacaca caaaaaaactt aaaagcacga acaacctaac    666
ttgaaaaara attttaaaat atgattaacc tgaaraaaar araatcctaa ragccaaagc    726
tccttttttat ttagcttgga attttcctat tggttcctaa caaactgtcc caatgtcata    786
taaggaaaca tgatctatta cattccttta taacaacgtg gararactat aaacctatgt    846
aagtagtaaa actatatcag adactcagga ractgactww aaggcctgga tctgcagtgt    906
attatctgta taaaaattgg cagggggaag ctaaaaggaa aggagattgg agatctcaat    966
tctatcatgg tgtatttcat acgcaaataca ragcatgcat tgttttttgt ttttggaar    1026
avaarggaag tgtgttctgc cccatgtttc ctcccggtgt tatagttcaa actctatata    1086
tacttcaggt attttttgtt tagcccttca ttataaatgg gcaggaaatt gtttatcaac    1146
ctagccaggt tattactagt gaccttgact tcagtatctt gagcattctt ttatatTTTT    1206
cttttattat cctgagtcgt taactaaaca attttgtctt caaattttta tccaatatcc    1266
attgcaccac accaaatcaa gcttcttgat tttcaaaaat aaaaaggggg aaatacttac    1326
aacttgtaaa aaaaaaaaaa
  
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<210> 329
 <211> 585
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 331..432

<220>
 <221> sig_peptide
 <222> 331..387
 <223> Von Heijne matrix
 score 7
 seq AGLSSCLLPLCWL/ER

<220>

<221> polyA_signal

<222> 548..553

<220>

<221> polyA_site

<222> 573..585

<400> 329

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aagcctaggt gtggcgcccc gaccggaatt tcacttctgg ccagcccttt cccacctgg      60
gcgcggggass ggtgccagtc tttaaacaac ctctcgatgg gtcccacgaa gatgtttcca    120
gacccttgga atgccaagtt caagtttagc tatgtctcgc ggagaggccg gtggaagaag    180
caacgagaat gaagcacccc agttctctgc tgagcacatg ggcattctgca ataaagattt    240
aatttcccag cttctcctga agctcggtat ggccacaaca cttaaattctg cccgaggaga    300
ttgagcaaaa tagtatggga cttccaagaa atg ttt tta aag tca ggg gca ggc      354
Met Phe Leu Lys Ser Gly Ala Gly
```

-15

```
ctt tct tca tgc ctt ctt cct ctt tgc tgg ctg gaa cgc aaa gac cat      402
Leu Ser Ser Cys Leu Leu Pro Leu Cys Trp Leu Glu Arg Lys Asp His
-10 -5 1 5
```

```
ggc agg agg cca agc asc cat cct gga agg tgaaagcctc atactaagga      452
Gly Arg Arg Pro Ser Xaa His Pro Gly Arg
```

10

15

```
cgtcaracag cgaaataara rcctgggtcc ttgaccctgt aaasatctcc ctccccatcc    512
tggtctgtct gccttgactc ctttcatatg aaaaaaataa acttttaact tgcgtwaacc    572
aaaaaaaaaa aaa      585
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<210> 330

<211> 914

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..703

<220>

<221> sig_peptide

<222> 59..220

<223> Von Heijne matrix
score 5.09999990463257
seq FLLSQMSQHQVHA/VQ

<220>

<221> polyA_signal

<222> 886..891

<220>

<221> polyA_site

<222> 903..914

<400> 330

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acaaatatca atgatgttta tgaatctagt gtgaaagtkt taatcacatc acaaggct      58
atg aac rra tat gca agt cca ttc aac tgw caa ttg ard tat ttg gak      106
Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
-50 -45 -40
ttg agc agr ttc gag tgt gtr cat aga gat gga aga gta att aca ctg      154
Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
```

	-35		-30		-25		
tct tat cag gag cag gag cta cag gat ttt ctt ctg tct cag atg tca						202	
Ser Tyr Gln Gln Gln Leu Gln Asp Phe Leu Leu Ser Gln Met Ser							
	-20		-15		-10		
cag cac cag gta cat gca gtt cag caa ctc gcc aag gtt atg ggc tgg						250	
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp							
	-5		1		5		10
caa gta ctg agc ttc agt aat cat gtg gga ctt gga cct ata gag agc						298	
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser							
	15		20		25		
abt ggt aat gca tct gcc atc acg gtg gcc ccc caa gtg gtg act atg						346	
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met							
	30		35		40		
cta ttt cag ttc gta atg gac ctg aaa gtg gca gca aga tta tgg ttc						394	
Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe							
	45		50		55		
agt ttc ctc gta acc aat gta aar acc ttc caa aaa gtg atg ttt tac						442	
Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr							
	60		65		70		
aar ata aca aat gga gtc atc ttc gtg ggc cat tca aar aag ttc agt						490	
Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser							
	75		80		85		90
gga ata aaa tgg aag gtc kaa att ttg ttt ata aaa tgg arm tgc tta						538	
Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu							
	95		100		105		
tgt ctg cac tta gcc ctt gtc tac tat gat ttt ttc car atg ttt cct						586	
Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro							
	110		115		120		
aaa raa gtt tcc ara aac ttt gac ttg aaa tgt ttg car atc aac tat						634	
Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr							
	125		130		135		
aag cac aaa gaa gar ata act tcc aaa aga gtg ctg ttt tta aaa ata						682	
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile							
	140		145		150		
ata att agg aaa tgt ttt att tagcactttc aaacttttca ctttataaat						733	
Ile Ile Arg Lys Cys Phe Ile							
	155		160				
gacaagtgct ttgaaatgca gaagtttatg tacagttgta tatacagtat gacaagatgt						793	
aaaataatat gtttttcatg cagtttaaaa tattactaac ttaagggttt ctatgtgctt						853	
tttaaaatat tccttctttg atgttgacat caaataaagt atgtgggttta aaaaaaaaaa						913	
a						914	

<210> 331
 <211> 1161
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 672..752

<220>
 <221> sig_peptide
 <222> 672..722
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LLYAHLSTSKRA/VV

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<220>
<221> polyA_site
<222> 1150..1161

<400> 331
aagatatcac tgtcttgttt tcaacttagat cctacttaca aagtgaggggt tattaacaga      60
ataaagcctt ccttttaaagc tttataataa tcatatttat taataatgct gttgtgcata      120
cttatagtat gcatatatcc agcatatggt gcatgtsttc agaattacat aagatgaaat      180
ccctttcatt gcaacttgca agtgagaaaa gatccttagt ggctctgggtg gaagaaatag      240
tattttcttct tctcaggggtg tctccctgcc ttggcccttc ccagaagccc cggcttttaa      300
agtgaaaatg tttgaaacat gaaacatgtc tgtaggaagc atcagcatgg ccataagtgc      360
artgattttc atatatgcct ctgcccattt caaatatatt tttgacatga ataaatctaa      420
cagtatacar aataattcat gtaaraccct aacgtgtaca tgtgaaaaag catttctata      480
taatgtgagg agcactggcc atcaattagg gaaataaagg tcatgtaata ttgcaaattt      540
tcaaaataga gcsstgcaag ataactgcaa tcataccaaa aactatttga gtaaattggat      600
ttttaaagta atttttgttt aaaaaaattt atatttcaga agsagaaaaat gtcaaattgat      660
agtctttgta a atg gtg gtg cac ctt ctc tat gca cat ctg tct ttt aca      710
                Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr
                -15                -10                -5
tca aaa aga gct gtg gtc atg cta aaa tta gag ata act ttt      752
Ser Lys Arg Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
                1                5                10
tgaatgactt ggtcaagctg tgtgtaaaat atttaacat aagtcaagta cagtgtacta      812
tgtttaataa agttacattt aatgcattta ttgcatatat gaatatatac atgaagaggc      872
tttatgtctt ctggtatttg attttgaatg ttttttaagt cagtgggtgcc tttaggcaag      932
aactttcgaa attaattcatt ctttgtgttt tctgattttt caggtaacat gtacactatt      992
tagaaacat catagtttat tcaccttaaa aaattgattg tattatttaa atatatact      1052
tagatgggca tttcctataa ttaggatatt ccaaatagtt gctgaaatca attgtgccat      1112
tgaccaatgg atgcacttgg tttagccttaa ttttttyaaa aaaaaaaaaa      1161

<210> 332
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..311

<220>
<221> sig_peptide
<222> 57..128
<223> Von Heijne matrix
      score 5.30000019073486
      seq LFHLLFLPHYIET/FK

<220>
<221> polyA_signal
<222> 332..337

<220>
<221> polyA_site
<222> 351..363

<400> 332
acattttctta ctgccttacg ctcatcctga ggtccacctt ggtctctaaa aacacc atg      59

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Asn Val Leu Gln Leu Pro Asn Phe	
30 35	
agtcaaaatg ttgccaaata tttatttcctt ttgcctaakt ttggctaccc ggttcaattg	322
cttttttattt ttaatgtctt gactcttcar agttcgtacc tcaaaaraac aatgaraaca	382
tttgctttgc tttctgctga atccctaate tcaacaatct atacctggac tgtccagttc	442
tcctcctgtg ctatcttctc ttctatccaa gtaraatgta ygccaggarc tccttccctc	502
tarcaatttc tactaaaatg tccaagtara atgtttcctt ttacaatcaa attactgtat	562
ttattaattt gctaraatcc aktaaateat tttggtagct ctggctgtgc tatcaataaa	622
aagatgaaag caaaaaaaaaaaa aaa	645

<210> 334
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..291

<220>
 <221> sig_peptide
 <222> 91..219
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LISVLYLIPKTLT/TN

<220>
 <221> polyA_signal
 <222> 367..372

<220>
 <221> polyA_site
 <222> 389..400

<400> 334	
aacaaaagga gagttttata attcacttta aaaggagatt tgatggtaaa gtttaaagat	60
taaaatattt tgttcttcaa ttacagagcg atg acc cca cag tat ctg cct cac	114
Met Thr Pro Gln Tyr Leu Pro His	
-40	
ggt gga aaa tac caa gtt ctt gga gat tac tct ttg gca gtg gtc ttc	162
Gly Gly Lys Tyr Gln Val Leu Gly Asp Tyr Ser Leu Ala Val Val Phe	
-35 -30 -25 -20	
ccc ctg cac ttt tct gat cta att tct gtt tta tac ctt ata ccc aaa	210
Pro Leu His Phe Ser Asp Leu Ile Ser Val Leu Tyr Leu Ile Pro Lys	
-15 -10 -5	
aca ctt act acc aac aca gct gtt aaa cat tct ata caa aaa aat tgt	258
Thr Leu Thr Thr Asn Thr Ala Val Lys His Ser Ile Gln Lys Asn Cys	
1 5 10	
atg mat ctg gta tta gga aaa tta ctt tca cag taaatatcaa agaaaaaaga	311
Met Xaa Leu Val Leu Gly Lys Leu Leu Ser Gln	
15 20	
ttaagggtct ctttgccatg cttttcatca tatgcaccaa atgtaaattt tgtacaataa	371
aattttattt cctaagyaaa aaaaaaaaaa	400

<210> 335
 <211> 496
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 196..384

<220>

<221> sig_peptide

<222> 196..240

<223> Von Heijne matrix

score 6.69999980926514

seq ILSTVTALTTFARA/LD

<220>

<221> polyA_signal

<222> 461..466

<220>

<221> polyA_site

<222> 485..496

<400> 335

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aaaaaattgg tcccagtttt caccctgccg cagggctggc tggggagggc agcggtttag    60
attagccgtg gcctaggccg tttaacgggg tgacacgagc htgcagggcc gagtccaagg    120
cccggagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag    180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt    231
               Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
               -15               -10               -5

gcc aga gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt    279
Ala Arg Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
               1               5               10

gag aag cac aga ctc gag aaa tgt agg gaa ctc gag agc agc cac tcg    327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser
               15               20               25

gcc cca gga tca acc cag cac cga aga aaa aca acc aga aga aat tat    375
Ala Pro Gly Ser Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
               30               35               40               45

tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc    424
Ser Ser Ala

atatttaaatt tggaaaagtc aaattgasca ttattaaata aagcttgttt aatatgtctc    484
aaacaaaaaa aa    496
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<210> 336

<211> 968

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 54..590

<220>

<221> sig_peptide

<222> 54..227

<223> Von Heijne matrix

score 3.5

seq GGILMGSFQGTIA/GQ

<220>
 <221> polyA_site
 <222> 955..965

<220>
 <221> misc_feature
 <222> 391
 <223> n=a, g, c or t

<400> 336
 atatttgccc cttactttat cttgtgcctt gagaaattgc tggggagaga ggt atg 56
 Met
 tcc act ggg cag ctg tac agg atg gag gat ata ggg cgt ttc cac tcc 104
 Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser
 -55 -50 -45
 cag cag cca ggt tcc ctg acc cca agc tca ccc act gtt ggg gag att 152
 Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile
 -40 -35 -30
 atc tac aat aac acc aga aac aca ttg ggg tgg att ggg ggt atc ctt 200
 Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu
 -25 -20 -15 -10
 atg ggt tct ttt cag gga acc att gct gga caa ggc aca gga gcc acc 248
 Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr
 -5 1 5
 tcc att tct gag ctg tgc aag gga caa gaa cta gag cca tca ggg gct 296
 Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala
 10 15 20
 ggg ctg act gtg gcc cca ccc caa gcc gtc agc ctg cag ggw atc tac 344
 Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile Tyr
 25 30 35
 acc ctg cct tgg ctg cta cag ctt ttt cac tcc act gcc cta rgg gna 392
 Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa Xaa
 40 45 50 55
 dtt cag caa cct aat gga tct cta tct ctg aac atc tct tca tcc cat 440
 Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser His
 60 65 70
 gct ccr rgt cca rca acc tgc acc ctg gaa cca gga gtg gac cct acc 488
 Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro Thr
 75 80 85
 cga sct gtc tgt att aat ccc cat ccc cca cca cca atc tta aaa abc 536
 Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys Xaa
 90 95 100
 cct ctg tcc ccc tac cct aaa ccc cag tta ggt acc cat gct ggg caa 584
 Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly Gln
 105 110 115
 gtc aat taacaattta tgcacaggta ctagttttat tgtattaccg ttccagggta 640
 Val Asn
 120
 gctttgaaaa aagtatctca aaaaggcaac atgggccgag cgcagtggct cacgcctgta 700
 atcccagcac tttgggaggc caaggtgggc agatcgccctg aggtctggag ttcaagacca 760
 gcctggccaa cagggtgaaa ccccgctctct acaaaaatar gaaaattrgc caggtgtggt 820
 ggcagacgtc tgtrgtccca gctattcagg agactgaggc acgagaattc catgaaccca 880
 ggatgctggag gttgcagtga gccgagattg tgccactgcg ctccagcctg ggcgacagag 940
 tgggtattctg tttcaaaaaa aaaaamcm 968

<210> 337

<211> 901
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..846

<220>
 <221> sig_peptide
 <222> 133..345
 <223> Von Heijne matrix
 score 9.39999961853027
 seq VVSFLLLLAGLIA/TY

<220>
 <221> polyA_site
 <222> 890..901

<220>
 <221> misc_feature
 <222> 72..73,138..140
 <223> n=a, g, c or t

<400> 337
 aagcagcttc caggatcctg agatccggag cagccgggggt cggagcgggt cctcaagagt 60
 tactgatcta tnnatggcag agaaaaaaaa attgtgacca gagacgtgta gcaatgaaca 120
 aggaacrtca ta atg rwn nnk ttc aca gac ccc tct tca gtg aat gaa aag 171
 Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
 -70 -65 -60
 aag agg agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag 219
 Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
 -55 -50 -45
 ccg ctc att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg 267
 Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu
 -40 -35 -30
 aag gaa tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct 315
 Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser
 -25 -20 -15
 ttt tta ctg ctg ctt gct ggg ctt ata gct acg tat tat gtt gaa gga 363
 Phe Leu Leu Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly
 -10 -5 1 5
 gtg cat caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat 411
 Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr
 10 15 20
 gcc tac tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca 459
 Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr
 25 30 35
 ggg ctg cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt 507
 Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val
 40 45 50
 aca tta gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc 555
 Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro
 55 60 65 70
 tat cct gat cag att att tgt cca gat gaa gag ggc act gaa gga acc 603
 Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr
 75 80 85

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att tct ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg      651
Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met
          90          95          100
tgg ggt atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc      699
Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala
          105          110          115
aga gca gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag      747
Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln
          120          125          130
gaa ttt gaa gag atg ctg gaa cat gca gag tct gca caa gta aga aca      795
Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr
          135          140          145          150
gtg ggg ata gaa aat aga aca ctt tac ttc ttc cta aag agg cta tta      843
Val Gly Ile Glu Asn Arg Thr Leu Tyr Phe Phe Leu Lys Arg Leu Leu
          155          160          165
agg taaaattggt agtagttact ctgaagaaga aaactgctaa agtaaaaaaa aaaaa      901
Arg

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<210> 338
<211> 1347
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 138..671

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<220>
<221> sig_peptide
<222> 138..248
<223> Von Heijne matrix
      score 3.5
      seq LVFNFLILTILT/IW

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<220>
<221> polyA_signal
<222> 1319..1324

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<220>
<221> polyA_site
<222> 1338..1347

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<400> 338
aagaatgctt gtgaagtagc aactaaagtg gcagtgtttc ttctgaaatt ctcaggcagt      60
cagactgtct taggcaaatc ttgataaaat agcccttata caggttttta tctaaggaat      120
cccaagaaga ctggggga atg gag aga cag tca agg gtt atg tca gaa aag      170
              Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys
              -35              -30
gat gag tat cag ttt caa cat cag gga gcg gtg gag ctg ctt gtc ttc      218
Asp Glu Tyr Gln Phe Gln His Gln Gly Ala Val Glu Leu Leu Val Phe
      -25              -20              -15
aat ttt ttg ctc atc ctt acc att ttg aca atc tgg tta ttt aaa aat      266
Asn Phe Leu Leu Ile Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn
      -10              -5              1              5
cat cga ttc cgc ttc ttg cat gaa act gga gga gca atg gtg tat ggc      314
His Arg Phe Arg Phe Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly
          10          15          20

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ctt aya atg gga cta att tta csa tat gct aca gca cca act gat att      362
Leu Xaa Met Gly Leu Ile Leu Xaa Tyr Ala Thr Ala Pro Thr Asp Ile
      25              30              35
gaa agt ggr rct gtc tat gac tgt gta aaa cta act ttc agt cca tca      410
Glu Ser Gly Xaa Val Tyr Asp Cys Val Lys Leu Thr Phe Ser Pro Ser
      40              45              50
act ctg ctg gtt aat atc act gac caa gtt tat gar tat aaa tac aar      458
Thr Leu Leu Val Asn Ile Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys
      55              60              65              70
aga gaa ata agt cag cac amc atc aat cct cat cam gga aat gct ata      506
Arg Glu Ile Ser Gln His Xaa Ile Asn Pro His Xaa Gly Asn Ala Ile
      75              80              85
ctt gaa aag atg aca ttt gat cca raa atc ttc ttc aat gtt tta ctg      554
Leu Glu Lys Met Thr Phe Asp Pro Xaa Ile Phe Phe Asn Val Leu Leu
      90              95              100
cca cca att ata ttt cat gca gga tat agt cta aag aag aga cac ttt      602
Pro Pro Ile Ile Phe His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe
      105              110              115
ttt caa aac tta gga tct att tta acg tat gcc ttc ttg gga act gcc      650
Phe Gln Asn Leu Gly Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala
      120              125              130
atc tcc tgc atc gtc ata ggg taagtgcacat tcggagctca agttgcaggt      701
Ile Ser Cys Ile Val Ile Gly
      135              140
ggctgtgggg tcygtgatct gtgtgagggg tctaacactt ccaggattct tgctggckgg      761
gaaaattgtc ttttttttar tawatcacaw atttgtatgt tttttcwgac ttaattccac      821
ggcttckgam aaatacaagg cttcaaataa aagcaaacta waggattgct ggactttctc      881
tgtgagttct ggacttctga cttagggaat gtggatcact tgccttgagt tatgtgaagc      941
gcattgcatt cttcttttag tttgagtaat sccgatatgc tcaactgcatt cttttttgtc      1001
ttgtattgag agaccttacc tgtatttggc aggagtgcac aagtaactat atgccaagag      1061
ttttctttct aaaggaaagt ttacaagaca gcagtctgaa acagatatgt ccaaatatca      1121
acagagttgc ttaatacagg gatagctttt cagttaatac cctgtagaat gcagactctt      1181
tttttcattg tattttcttg attatgctac tgagccctaa gtcacacggt atatactctg      1241
gcttgcagct catcataaag taaaatgtgg taccaaattg tgaaggcaat ccagcctctg      1301
ataatcccgct ccaatacatt aaagctccac tgcaggaaaa aaaaaa      1347

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<210> 339
<211> 987
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 124..411

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<220>
<221> sig_peptide
<222> 124..186
<223> Von Heijne matrix
      score 6.30000019073486
      seq MVALCCCLWKISG/CE

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<220>
<221> polyA_signal
<222> 948..953

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<220>

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<221> polyA_site

<222> 971..983

<400> 339

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aagacgctgc ctttagggag agataaaaag cataatgaca ttagctagga aagttaattt    60
tcagttctta ctgaagtgct gtatgaaact gaaatttcca aggaactgaa ttttgtgagc    120
caa atg agc atg caa ttc ttg ttt aag atg gtg gcc tta tgc tgt tgt    168
   Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys
      -20                -15                -10
ctc tgg aag atc tcc ggc tgt gag gaa gtc cct cta act tac aac ctg    216
Leu Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu
   -5                1                5                10
ctc aag tgc ctc cta gat aaa gcg cac tgt gta ctc ctg aca cct tgt    264
Leu Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys
      15                20                25
ggg tac atc ttt tcc ttg atc agt cca gaa att ctc aaa ctc act tta    312
Gly Tyr Ile Phe Ser Leu Ile Ser Pro Glu Ile Leu Lys Leu Thr Leu
      30                35                40
atc act ttg cav atc ctc tta ata ctc aaa aat cta cac tta ctg tgg    360
Ile Thr Leu Xaa Ile Leu Leu Ile Leu Lys Asn Leu His Leu Leu Trp
      45                50                55
ctg aca gtt tca agc awa tgt gtt cat cgc agt agt gca aga aaa gaa    408
Leu Thr Val Ser Ser Xaa Cys Val His Arg Ser Ser Ala Arg Lys Glu
      60                65                70
aag tagaagaacc ctgcagagat ttgatggaac ccagcttcta ttcattaaaa    461
Lys
75
ccaatggcaa aatataaagc aaataggagg tgacgaaggt tacaaaaata cgtattgttt    521
atgttttccc tgggggtgtgc tgattgtcag gcatcagttc cctgtgccat tcattcccca    581
acacagcatg catcagaaat tttatcaata aatgctttct ctctcaatgt tcaacctatg    641
ctgatagacc attaaataca gtttttgggt tcacagcttg tcatcatcat ttgtctatac    701
ctgtggcaaa gaatatctaa taagatactc tcagcatttt gcacacttaa actaagatgc    761
tgaatgctgt attttacgga ataatcagcc acattaaatt tggagactca acaagcatgc    821
tgtgaacatt caacattagg tttaaatttt atttttaaaa gttaataata aaaggatata    881
tgттаagtat tatgaaaccc tgcataact gtaataaaat ggtggatgtg aatggacaat    941
atatgcaata aaatttataa tttgattcya aaaaaaaaaa aamccv    987
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<210> 340

<211> 748

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 372..494

<220>

<221> sig_peptide

<222> 372..443

<223> Von Heijne matrix

score 5.30000019073486

seq RILLHIFYCLLR/SE

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<221> polyA_signal

<222> 708..713

<220>
 <221> polyA_site
 <222> 732..745

<400> 340
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 tgaggttggt taattcagct ggccctggct cctgggccct gttactgagc tgggcagtcg 120
 aaccgaaggc agatgagctc aagatcatgc cttgggaagc atgggtgctct aggggtgcct 180
 ttttattcct ttcattgtat tatagactgt ttccaagttt atgggttagaa atggtaaagt 240
 ggggtctggtg ttttgaggta gaaccagcc tagggcaaga tatgaactgt tcttgaggta 300
 gaaatgtcta cagtcagttg tttcatctag cttgcatctt aaaacacaaa cccttcagtt 360
 gctttcactt a atg cac aca ttt gcc aat gac aga ggg tta tac agg atc 410
 Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile
 -20 -15
 ctt ctt tta cat ttc tat tgt ctg cta cgc tca tca gag tat att ttg 458
 Leu Leu Leu His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu
 -10 -5 1 5
 ggg tac aag gtt ttg ggg gtt ttt tty ccc att ttg taactgcctt 504
 Gly Tyr Lys Val Leu Gly Val Phe Phe Pro Ile Leu
 10 15
 attgaaaadt aaktgccctt ccattccagg cctcctcata ttgtacttgt ttcttgccaa 564
 atctggggga tcatttgtat ttttaactttg taatctatgg ctctgtactg ttgaaagstc 624
 tcaattctgt ggggtctcct tagtatgtat gtgacttttc atgttgcaat atcacacgat 684
 gggatggccc gacttttgct cttaataaat aatctgaatg agtaagaraa aaaaaaaaaa 744
 accc 748

<210> 341
 <211> 1106
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..450

<220>
 <221> sig_peptide
 <222> 112..192
 <223> Von Heijne matrix
 score 7.19999980926514
 seq SLLFFLLLEGGXT/EQ

<220>
 <221> polyA_signal
 <222> 1053..1058

<220>
 <221> polyA_site
 <222> 1095..1106

<220>
 <221> misc_feature
 <222> 73..76,204
 <223> n=a, g, c or t

<400> 341
 aagacctcgg aacgagagcg ccccggggag ctcggagcgc gtgcacgcgt ggcavacgga 60

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gaaggcvakk rcnnnnrctt gaaggttctg tcaccttttg cagtgggtcca a atg aga      117
                                   Met Arg
raa aag tgg aaa atg gga ggc atg aaa tac atc ttt tgc ttg ttg ttc      165
Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
-25                               -20                               -15                               -10
ttt ctt ttg cta gaa gga ggc kaa aca gag caa gtr amn cat tca gag      213
Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu
                               -5                               1                               5
aca tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg      261
Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp
                               10                               15                               20
cat cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc      309
His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile
                               25                               30                               35
tgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat      357
Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn
40                               45                               50                               55
gtt cat tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc      405
Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg
                               60                               65                               70
tgc cca gaa gac tcc tta ccc cca gtg aac aat rwg gtg acc agc      450
Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr Ser
                               75                               80                               85
tagtcttgck agtacaatgg gacaacttac caacatggas agctgttcgt agctgrrggg      510
ctcttttcaga atcggaacc cmatcaatgc acccagtga gctgttcgga rggaaackt      570
tattgtggtc tcaagacttg ccccaaatta acctgtgcct tcccagtctc tgttccarat      630
tcctgctgcc gggwtgacag argagatgga caactgtcat gggaacmttc tgatgggtat      690
atcttcgggc aacctgcca cagagaagca agacattctt accaccgctc tcaactatgat      750
cctccacca ggcgacaggc tggaggtctg tcccgcttct ctggggccag aagtcaccgg      810
ggagctctta tggattccca gcaagcatca ggaaccattg tgcaaattgt catcaataac      870
aaacacaagc atggacaagt gtgtgtttcc aatggaaaga cctattctca tggcgagtcc      930
tggcacccaa acctccgggc atttggcatt gtggagtgtg tgctatgtac ttgtaatgtc      990
accaagcaag agtgaagaa aatccactgc cccaatcgat acccctgcaa gtatcctcaa     1050
aaaatagacg gaaaatgctg caaggtgtgt ccaggtaaaa aagcaaaaaa aaaaaa     1106

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<210> 342
<211> 1191
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 117..866

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<220>
<221> sig_peptide
<222> 117..170
<223> Von Heijne matrix
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      seq LILLALATGLVGG/ET

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<222> 1159..1164

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<220>
<221> polyA_site

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<222> 1178..1190

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<221> misc_feature

<222> 67

<223> n=a, g, c or t

<400> 342

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agagcbnmag cccagagcc taggaacctg gggcccgctc ctccccctc caggcc atg 119
Met
agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg 167
Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly
-15 -10 -5
gga gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag 215
Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln
1 5 10 15
ccc tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg 263
Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
20 25 30
acg ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag 311
Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
35 40 45
ccc cgc tac ata ktt cac ctg ggg cag cac aac ctc cag aag gag gag 359
Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu Glu
50 55 60
ggc tgt gag car acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc 407
Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly
65 70 75
ttc aac aac agc ctc ccc aac aaa gac cam mgc aat gac atc atg ctg 455
Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met Leu
80 85 90 95
gtg aak atg gma tgc cca gtc tcc atc acc tgg gct gtg cga ccc ctc 503
Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu
100 105 110
acc ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc 551
Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser
115 120 125
ggc tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg 599
Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu
130 135 140
cga tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc 647
Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala
145 150 155
tac ccc ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa 695
Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu
160 165 170 175
ggg ggc aag gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt 743
Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
180 185 190
aac cag tct ctt caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg 791
Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
195 200 205
atc acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat gtg gac 839
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp
210 215 220
tgg atc cag gag acg atg aag aac aat tagactggac ccacccacca 886
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Trp Ile Gln Glu Thr Met Lys Asn Asn

225	230		
cagcccatca	ccctccattt	ccacttggtg	tttggttcct
gttcactctg	ttaataagaa		946
accctaagcc	aagaccctct	acgaacattc	tttgggcctc
ctggactaca	ggagatgctg		1006
tcacttaata	atcaacctgg	ggttcgaaat	cagtgaagacc
tggattcaaa	ttctgccttg		1066
aaatattgtg	actctgggaa	tgacaacacc	tggtttgttc
tctgttgat	ccccagcccc		1126
aaakwcagct	cctggccata	tatcaagggt	tcaataaata
tttgctaaat	gaawaaaaaa		1186
aaaac			1191

<210> 343
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 13..465

<220>
 <221> sig_peptide
 <222> 13..75
 <223> Von Heijne matrix
 score 3.90000009536743
 seq PVAVTAAPVLS/IN

<220>
 <221> polyA_signal
 <222> 1035..1040

<220>
 <221> polyA_site
 <222> 1060..1070

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Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr	
-20 -15 -10	
gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg	99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu	
-5 1 5	
cg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cg gag	147
Arg Glu Ile Lys Lys Gln Leu Leu Ile Ala Gly Leu Thr Arg Glu	
10 15 20	
cg ggc cta cta cac agt agc aaa tgg tgc gcg gag ttg gct ttc tct	195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser	
25 30 35 40	
ctc cct gca ttg cct ctg gcc gag ctg caa ccg cct ccg cct att aca	243
Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr	
45 50 55	
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac	291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr	
60 65 70	
ttt gac gtt aaa gag tat gat cg gca gca cat ttc ctg cat ggc tgc	339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys	
75 80 85	
aat gca aga aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg	387
Asn Ala Arg Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val	


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      90              95              100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
105              110              115              120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtggggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
      125              130
gaatgaatgt actttataca tagcaataat aaaaaaaaga tatkataaat aaagttaaaa      545
aggatggtaa aaaaaaaaaat attcttagga atgactaaca ggataagtaa caacctgatt      605
atttattttac tttagggttat ataagggttct tcatgcctgt gaattaatat tattgtgtaa      665
gaattaagtt aaaaagcctg ggctgacttt taaatttata aattcattta tcatgtttat      725
agtatatttta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca      785
agtaaaccac ctttaactctg tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tactttccta ctttttctta gttgttatct atataaattg attaaaaaaa      905
cattttatgt actttctcatt tcctagtaga gggtgagtag cccttatttg aagtgtttgg      965
gaccaaaggt gtttcagatt tcagattttt ttcagatttt ggtatatttg cattataact      1025
actggttgaa ataaaaaatg ctgcagtgag tgtcaaaaaa aaaaaa      1070

<210> 344
<211> 1213
<212> DNA
<213> Homo sapiens

<220>
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<222> 2..718

<220>
<221> sig_peptide
<222> 2..76
<223> Von Heijne matrix
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      seq RVGLLLGGGGVYG/SR

<220>
<221> polyA_signal
<222> 1170..1175

<220>
<221> polyA_site
<222> 1203..1213

<400> 344
a atg ccc cgg aag cgg aag tgc gat ctt cgg gct gtc aga gtt ggt ctg      49
  Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
   -25              -20              -15              -10
tta ctc ggt ggt ggc gga gtc tac gga agc cgt ttt cgc ttc act ttt      97
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
              -5              1              5
cct ggc tgt aga gcg ctt tcc ccc tgg cgg gtg aga vtg cag aga cga      145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
      10              15              20
agg tgc gag atg agc act atg ttc gcg gac act ctc ctc atc gtt ttt      193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
      25              30              35
atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg gtc ctg      241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu

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40		45		50		55	
ggt	tac	agg	aca	gac	aag	tac	aag
Val	Tyr	Arg	Thr	Asp	Lys	Tyr	Lys
			60			65	
cag	agt	aaa	aaa	ttg	gaa	aag	aag
Gln	Ser	Lys	Lys	Leu	Glu	Lys	Lys
			75			80	
ggt	cga	caa	cag	aaa	aar	aaa	ata
Gly	Arg	Gln	Gln	Lys	Lys	Lys	Ile
			90			95	
aat	aac	aac	aga	gat	cta	tca	atg
Asn	Asn	Asn	Arg	Asp	Leu	Ser	Met
			105			110	
att	ggc	ttt	tgt	ttt	act	gcc	cta
Ile	Gly	Phe	Cys	Phe	Thr	Ala	Leu
			120			125	
gat	ggt	aga	gtg	gtg	gca	aag	ctt
Asp	Gly	Arg	Val	Val	Ala	Lys	Leu
			140			145	
sra	gga	ctg	tct	cat	cga	aat	ctg
Xaa	Gly	Leu	Ser	His	Arg	Asn	Leu
			155			160	
tcc	ttc	att	ttc	ctg	taw	att	ctc
Ser	Phe	Ile	Phe	Leu	Xaa	Ile	Leu
			170			175	
att	cag	aag	att	ctc	ggc	ctt	gcc
Ile	Gln	Lys	Ile	Leu	Gly	Leu	Ala
			185			190	
gca	ggt	gga	ttt	ctt	ggc	cca	cca
Ala	Gly	Gly	Phe	Leu	Gly	Pro	Pro
			200			205	
							210
tgaactcaag	aactctttat	tttctakcat	tcttttctaga	cacacacaca	tcagactggc		778
aactgttttg	tascaagagc	cataggtagc	cttackactt	gggcctcttt	ctagttttga		838
attattttcta	agccttttgg	gtatkattag	agtgaaaatg	gcagccagca	aacttgatag		898
tgcttttggg	cctagatgat	ttttatcaaa	taagtggatt	gattagttaa	gttcaggtaa		958
tgttttatgta	atgaaaaaca	aatagcatcc	ttcttgtttc	atttacataa	gtattttctg		1018
tgggaccgac	tctcaaggca	ctgtgtatgc	cctgcaagtt	ggctgtctat	gagcatttag		1078
agatttagaa	gaaaaattta	gtttgtttta	cccttgtaac	tgtttgtttt	gttggtggtt		1138
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atgtaaaaaa	aaaaa						1213

<210> 345
 <211> 978
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 86..709

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 <222> 86..361
 <223> Von Heijne matrix
 score 6.30000019073486
 seq LLMSILALIFIMG/NS

<220>
 <221> polyA_signal
 <222> 943..948

<220>
 <221> polyA_site
 <222> 963..973

<220>
 <221> misc_feature
 <222> 469
 <223> n=a, g, c or t

<400> 345
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 ggacgaaaga gtcggcgccg ccgta atg cga gag ccg cag aag aga acc gca 112
 Met Arg Glu Pro Gln Lys Arg Thr Ala
 -90 -85
 aca atc gca aaa tyc rrg gcs tva gag ggc ctc cga gac ccc tat ggc 160
 Thr Ile Ala Lys Xaa Xaa Ala Xaa Glu Gly Leu Arg Asp Pro Tyr Gly
 -80 -75 -70
 cgc ctc tgt ggt agc gag cac ccc cga aga cca cct gag cgg ccc gag 208
 Arg Leu Cys Gly Ser Glu His Pro Arg Arg Pro Pro Glu Arg Pro Glu
 -65 -60 -55
 gaa gac ccg agc act cca gag gag gcc tct acc acc cct gaa gaa gcc 256
 Glu Asp Pro Ser Thr Pro Glu Glu Ala Ser Thr Thr Pro Glu Glu Ala
 -50 -45 -40
 tcg agc act gcc caa gca caa aag cct tca gtg ccc cgg agc aat ttt 304
 Ser Ser Thr Ala Gln Ala Gln Lys Pro Ser Val Pro Arg Ser Asn Phe
 -35 -30 -25 -20
 cag ggc acc aag aaa agt ctc ctg atg tct ata tta gcg ctc atc ttc 352
 Gln Gly Thr Lys Lys Ser Leu Leu Met Ser Ile Leu Ala Leu Ile Phe
 -15 -10 -5
 atc atg ggc aac agc gcc aag gaa gct ctg gtc tgg aaa gtg ctg ggg 400
 Ile Met Gly Asn Ser Ala Lys Glu Ala Leu Val Trp Lys Val Leu Gly
 1 5 10
 aag tta gga atg cag cct gga cgt cas cac agc atc ttt gga gat ccg 448
 Lys Leu Gly Met Gln Pro Gly Arg Xaa His Ser Ile Phe Gly Asp Pro
 15 20 25
 aag aar atc gtc aca gaa ran ttt gtg cgc aga ggg tac ctg att tat 496
 Lys Lys Ile Val Thr Glu Xaa Phe Val Arg Arg Gly Tyr Leu Ile Tyr
 30 35 40 45
 ara ccg gtg ccc cgt abc agt ccg gtg gag tat gas ttc ttc tgg ggg 544
 Xaa Pro Val Pro Arg Xaa Ser Pro Val Glu Tyr Xaa Phe Phe Trp Gly
 50 55 60
 ccc cga gca cac gtg gaa tcg agc ara ctg aaa stc wtg cat ttt gtg 592
 Pro Arg Ala His Val Glu Ser Ser Xaa Leu Lys Xaa Xaa His Phe Val
 65 70 75
 gca agg gtt cgt aac cga tgc tct aaa gac tgg cct tgt aat tat gac 640
 Ala Arg Val Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp
 80 85 90
 tgg gat tcg gac gat gat gca gag gtt gag gct atc ctc aat tca ggt 688
 Trp Asp Ser Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly
 95 100 105
 gct arg ggt tat tcc gcc cct taagtaratc tgaggcagac ccttgggggt 739
 Ala Xaa Gly Tyr Ser Ala Pro
 110 115

gtaaaagaga gtcacaggt	cccccaaggag tagatgccag	ggtcctaagt tgaaaatgmt	799
gtcgaattggg ggcgggggac	actgtatttg atatttgtga	tcagtgatca ttgttcaact	859
gcgaaataga gtgtttgctt	ttgataatgg aaaattgtat	tcgtttttaa attccgtttg	919
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<210> 346
 <211> 810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..320

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 <222> 63..179
 <223> Von Heijne matrix
 score 3.90000009536743
 seq VLAIGLLHIVLLS/IP

<220>
 <221> polyA_signal
 <222> 771..776

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gg atg aat gtk ggc aca gcg cac ags dag gtg aac ccc aac acg cgg	107
Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg	
-35 -30 -25	
gtk atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt	155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly	
-20 -15 -10	
ctc ctc cac atc gtg ctg ctg agc atc ccg ttt gtk agt gtc cct gtc	203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val	
-5 1 5	
gtc tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc	251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe	
10 15 20	
ctg cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag	299
Leu His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys	
25 30 35 40	
gcg agg ctg cta acc cac tgg tgagcagatg gattatgggg tccagttcac	350
Ala Arg Leu Leu Thr His Trp	
45	
ggcctctcgg aaktctctga ccatcacacc catcgtgctg tacttcctca ccagcttcta	410
cactaaktac raccaaattc attttgtgct caacaccgtg tccctgatra gcgtgcttat	470
ccccaaactg cccagctcc acggaktccg gatttttggg atcaataakt actgaaaktg	530
casccccctt ccctgccag ggtggcaggg gaggggtagg gtaaaaggca tktgctgcaa	590
chctgaaaac araaaraara rscctctgga cactgccara ratggggggt gagcctctgg	650
cctaatttcc cccctcgctt cccccagtag ccaacttgga gtagcttgta ytggggttgg	710
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<210> 347
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 <222> 299..418

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 <222> 299..379
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LLLLLITPSPSPL/LF

<220>
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 <222> 739..744

<220>
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 <222> 762..771

<400> 347
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 aaatgatgtc catttgagcc ccaccacgga ggttatgtgg tcccaaaagg aatgatggcc 180
 aagcaattaa tttttcctcc tagttcttag cttgcttctg cattgattgg ctttacacaa 240
 ctggcattta gtctgcatta cacaaataga cactaattta tttggaacaa gcagcaaa 298
 atg aga act tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act 346
 Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15
 ctg ctt cta atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt 394
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5
 ctg tcc ctc aga tca gca atg tct tagccctctt cctctcttcc attccttctt 448
 Leu Ser Leu Arg Ser Ala Met Ser
 10
 gttggtactc atttcttcta actttttaata aacatttagg tataatacat tacagtaagt 508
 gctattttaga tacaaactta aaacatacta tatatttttaa ggatctaaga atcctttara 568
 rrrggcacat gactgaagta cctcagctgc gcagcctgta accagttttt ttaatgtaaa 628
 agtaaraatg ccagccttaa cctabccctg carataaaag ctaactttta ttaataccag 688
 ccctgaataa tggcactaat ccacactctt ccttaragtg atgctggaaa aataaaatca 748
 ggggcttcag attaaaaaaa aaa 771

<210> 348
 <211> 409
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 186..380

<220>

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<221> sig_peptide
<222> 186..233
<223> Von Heijne matrix
      score 4
      seq FFLFLSFVLMYDG/LR

<220>
<221> polyA_signal
<222> 383..388

<220>
<221> polyA_site
<222> 396..409

<400> 348
ataaaagaag cagcaaatag aatttcccac aaagtaagtt gactctaaat cttaagtatt      60
acctagtttt ttaaagggtt gaatataata atgcagtatt tgcagtataa aaaggaagga      120
atttgtagag aatcattttg gtgctcaagt ctcttagcag tgccttattg cctcatagca      180
agaag atg ctg ggg ttt ttt ttg ttt ttg tcc ttt gta tta atg tat gat      230
      Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
            -15                    -10                    -5
ggt ttg cgc ctt ttt ggc att ctt tca aca tgt cgt gta cat cac acc      278
Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
      1              5              10              15
atg aat cag ttc cta att gat ata tct agc ttt acc tcc cga gtt aaa      326
Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Lys
            20              25              30
aaa aaa atc ttt tta ttt tat gcc ttc awa ggt tgc ycg ttt car agt      374
Lys Lys Ile Phe Leu Phe Tyr Ala Phe Xaa Gly Cys Xaa Phe Gln Ser
            35              40              45
gcc aca taaataaaat gtttaacaaa aaaaaaaaaa      409
Ala Thr

<210> 349
<211> 613
<212> DNA
<213> Homo sapiens

<220>
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<222> 69..458

<220>
<221> sig_peptide
<222> 69..233
<223> Von Heijne matrix
      score 4
      seq AALCGISLSQLFP/EP

<220>
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<222> 564..569

<220>
<221> polyA_site
<222> 602..613

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<220>
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 <222> 97
 <223> n=a, g, c or t

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 cgctggga atg gcc atg tgg aac agg cca tgb bag ang ctg cct cag cag 110
 Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln
 -55 -50 -45
 cct cts sta gct gag ccc act gca gag ggg gag cca cac ctg ccc acg 158
 Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr
 -40 -35 -30
 ggc cgg gas byg act gag gcc aac cgc ttc gcc tat gct gcc ctc tgt 206
 Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
 -25 -20 -15 -10
 ggc atc tcc ctg tcc cag tta ttt cct gaa ccc gaa cac agc tcc ttc 254
 Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
 -5 1 5
 tgc aca gag ttc atg gca ggc ctg gtg ckm tgg ctg gag ttg tct gaa 302
 Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
 10 15 20
 gct gtc ttg cca acc atg act gct ttt gcg agc ggc ctg gga ggt gaa 350
 Ala Val Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu
 25 30 35
 gga sca vma tgt gtt tgt tca aat ttt act gaa gga ccc cat ctt gaa 398
 Gly Xaa Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu
 40 45 50 55
 gga cga ccc gac ggt gat cac tca gga cct tct gag ctt ctc act caa 446
 Gly Arg Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln
 60 65 70
 gga tgg gca cta tgacscgg gccagagtc tcgtttgcc catgacctcc 498
 Gly Trp Ala Leu
 75
 ctgctccaag tgcccttggg gagctggat gtccttgaaa agatgttctt ggagagcctg 558
 aaggaaatca aagaagagga atctgaaatg gccgaggcat cccraaaaaa aaaaa 613

<210> 350
 <211> 986
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..638

<220>
 <221> sig_peptide
 <222> 12..263
 <223> Von Heijne matrix
 score 4.19999980926514
 seq ITMLQMLALLGYG/LF

<220>
 <221> polyA_signal
 <222> 951..956

<220>
 <221> polyA_site
 <222> 975..985

<400> 350

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      Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr
                        -80                        -75

gga cct ctc atg ctg gtc ttc act ctg gtt gct atc cta ctc cat ggg      98
Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly
      -70                        -65                        -60

atg aag acg tct gac act att atc cgg gag ggc acc ctg atg ggc aca      146
Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr
      -55                        -50                        -45                        -40

gcc att ggc acc tgc ttc ggc tac tgg ctg gga gtc tca tcc ttc att      194
Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile
                        -35                        -30                        -25

tac ttc ctt gcc tac ctg tgc aac gcc cag atc acc atg ctg cag atg      242
Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met
      -20                        -15                        -10

ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat tgc att gtc ctg ttc      290
Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe
      -5                        1                        5

atc acc tat aat atc cac ctc cgc gcc ctc ttc tac ctc ttc tgg ctg      338
Ile Thr Tyr Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu
      10                        15                        20                        25

ttg gtg ggt gga ctg tcc aca ctg cgc atg gta gca gtg ttg gtg tct      386
Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser
      30                        35                        40

cgg acc gtg ggc ccc aca cad cgg mtg ctc ctc tgt ggc acc ctg gct      434
Arg Thr Val Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala
      45                        50                        55

gcc cta cac atg ctc ttc ctg ctc tat ctg cat ttt gcc tac cac aaa      482
Ala Leu His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys
      60                        65                        70

dtg gta dag ggg atc ctg gac aca ctg gag ggc ccc aac atc ccg ccc      530
Xaa Val Xaa Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro
      75                        80                        85

atc cag agg gtc ccc aga gac atc cct gcc atg ctc cct gct gct cgg      578
Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg
      90                        95                        100                        105

ctt ccc acc acc gtc ctc aac gcc aca gcc aaa gct gtt gcg gtg acc      626
Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr
      110                        115                        120

ctg cag tca cac tgacccacc tgaaattctt ggccagtcct ctttcccga      678
Leu Gln Ser His
      125

gctgcagaga ggargaasac tattaaagga cagtcctgat gacatgtttc gtagatgggg      738
tttgacgtg ccaactgagct gtagctgctg aagtacctcc ttgatgcctg tcggcacttc      798
tgaaaggcac aaggccaaga actcctggcc aggactgcaa ggctctgcag ccaatgcaga      858
aaatgggtca gtcctttga gaacccctcc ccacctaccc cttccttcct ctttatctct      918
cccacattgt cttgctaaat atagacttgg taattaaaat gttgattgaa gtctggaaaa      978
aaaaaaaaat                                                                986

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<210> 351
 <211> 1447
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 282..389

<220>

<221> sig_peptide

<222> 282..332

<223> Von Heijne matrix

score 3.5

seq RWWCFHLQAEASA/HP

<220>

<221> polyA_signal

<222> 1413..1418

<220>

<221> polyA_site

<222> 1437..1447

<400> 351

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tggtctgkt	ctgacacctt	tccagaaaa	agtcaattgt	tcaggtagac	caaagaggaa	120
gaagagctgt	ggaggccacc	ctctacaaag	ctttatagaa	cttctggatc	taactcacia	180
acaagcttcc	agaagagact	agagacctta	ggccaggaga	tgaaggagtt	cagtagcaaa	240
gtcacacctg	tccaattccc	tgagctttgc	tcaactcagct	a atg gga tgg caa agg		296
				Met Gly Trp Gln Arg		
				-15		

tgg tgg tgc ttt cat ctt cag gca gaa gcc tct gcc cat ccc cct caa	344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln	
-10 -5 1	

ggg ctg cag gcc caa ttc tca tgc tgc cct tgg gtg ggc atc tgt	389
Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp Val Gly Ile Cys	
5 10 15	

taacaaadga	aaacgtctgg	gtggcggcag	casctttgct	ctgagtgcct	acaaagctaa	449
tgcttggtgc	tagaaacatc	atcattatta	aacttcagaa	aagcagcagc	catgttcagt	509
caggctcatg	ctgcctcact	gcttaagtgc	ctgcaggagc	cgcttgccaa	rtcccccttc	569
ctacacctgg	caactgggg	tctgcacaag	gctttgtcaa	ccaaaracag	cttccccww	629
ttgattgcct	gtagactttg	gagccaaraa	acactctgtg	tgactctaca	cacacttcag	689
gtggtttctg	cttcaaagtc	attgatgcaa	cttgaaagga	aacagtttaa	tggtggaaat	749
gaactaccat	ttataacttc	tgttttttta	ttgagaaaat	gattcacgaa	kkccaaatca	809
gattgccagg	aagaaatagg	acgtgacggg	actgggccct	gtgattctcc	cagcccttgc	869
agtccgctag	gtgagaggaa	aagctcttta	cttcgcgcct	tggcagggac	ttctgggtta	929
tgggagaaac	cagagatggg	aatgaggaaa	atatgaacta	cagcagaagc	ccctgggcag	989
ctgtgatgga	gcccctgaca	ttactcttct	tgcactctgc	ctgccttctt	tcctcttgcg	1049
aggcagtggg	gtgggattca	gagtgcctag	tctgctcact	gggagaagaa	gagttcctgc	1109
gcatgcaagc	cctgctgtgt	ggctgtcggt	tacatttggt	aggtgtcctg	tatgtctgta	1169
cgttggggac	tgctgttatt	tggaagattt	aaaaacctag	catcctgttc	tcacctctca	1229
agctgcattg	agaaatgact	cgtctctgta	tttgtattaa	gccttaacac	ttttcttaag	1289
tgcattcggt	gccaacattt	tttagagctg	tacaaaacaa	aaaagcctgt	actcacatca	1349
camtgtcatt	ttgataggag	cgtttttgta	tttttacaag	gcagaatggg	gtgtaacagt	1409
tgaattaaac	ttagcaatca	cgtgctcaaa	aaaaaaaa			1447

<210> 352

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 208..339

<220>

<221> sig_peptide

<222> 208..294

<223> Von Heijne matrix

score 5.59999990463257

seq LFLQLLSHEIVC/AT

<220>

<221> polyA_site

<222> 1631..1641

<400> 352

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atgatcatgc	agaggcagaa	gccaggcacc	tgggtctatga	atcagaccaa	aacaaggatg	120
gcaagcttac	caaggaggag	atcgttgaca	agtatgactt	atttgttggc	agccaggcca	180
cagattttgg	ggaggcctta	gtacggc atg	atg agt tct	gag cta	cgg agg aac	234
		Met Met	Ser Ser	Glu Leu	Arg Arg Asn	

-25

cct cat ttc	ctc aaa	agt aat	tta ttt	tta cag	ctt ctg	gtt tca	cat	282
Pro His	Phe Leu	Lys Ser	Asn Leu	Phe Leu	Gln Leu	Leu Val	Ser His	

-20

-15

-10

-5

gaa att gtt	tgc gct	act gag	act gtt	act aca	aac ttt	tta aga	cat	330
Glu Ile	Val Cys	Ala Thr	Glu Thr	Val Thr	Thr Asn	Phe Leu	Arg His	

1

5

10

gaa aag	gcg taatgaaaac	catcccgtcc	ccattcctcc	tcctctctga	379
Glu Lys	Ala				

15

gggactggag	ggaagccgtg	cttctgagga	acaactctaa	ttagtacact	tgtgtttgta	439
ratttacacw	wtgtattatg	tattaacatg	gcgtgtttat	ttttgtattt	ttctctgggt	499
gggagtatka	tatgaaggat	caaratcctc	aactcacaca	tgtaracaaa	cattasctct	559
ttactctttc	tcaacccctt	wtatgatttt	aataattctc	acttaactaa	ttttgtaagc	619
ctgagatcaa	taagaaatgt	tcaggagaga	ggaaagaaaa	aaaatatatg	ctccacaatt	679
tatatttaga	gagagaacac	ttagtcttgc	ctgtcaaaaa	gtccaacatt	tcataggtag	739
taggggccac	atattacatt	cagttgctat	aggtccagca	actgaacctg	ccattacctg	799
ggcaaggaaa	gatccctttg	ctctaggaaa	gcttggccca	aattgatttt	cttctttttc	859
cccctgtagg	actgactggt	ggctaatttt	gtcaagcaca	gctgtggtgg	gaagagttag	919
ggccagtgtc	ttgaaaatca	atcaagtagt	gaatgtgatc	tctttgcara	gctatagata	979
gaaacagctg	gaaaactaaa	ggaaaaatac	aagtgttttc	ggggcataca	ttttttttct	1039
gggtgtgcat	ctgttgaaat	gctcaagact	taattatttg	ccttttgaaa	tcactgtaaa	1099
tgcccccatc	cggttcctct	tcttcccarg	tgtgccaagg	aattaatctt	ggtttcacta	1159
caattaaaat	tcactccttt	ccaatcatgt	cattgaaagt	gcctttaacg	aaagaaatgg	1219
tcactgaatg	ggaattctct	taagaaaccc	tgagattaaa	aaaagactat	ttggataact	1279
tataggaaaag	cctagaacct	cccagtagag	tggggatttt	tttcttcttc	cctttctctt	1339
ttggacaata	gttaaattag	cagtattagt	tatgagtttg	gttgcaagtgt	tcttatcttg	1399
tgggctgatt	tccaaaaacc	acatgctgct	gaattttacca	gggatcctca	tacctcacia	1459
tgcaaacacc	ttactaccag	gcctttttct	gtgtccactg	gagagcttga	gtcacactc	1519
aaagatcaga	ggacctacag	agagggtctc	ttggtttgag	gacctgggt	tacctttcct	1579
gcctttgacc	catcacaccc	catttcctcc	tctttccctc	tccccgtgc	caaaaaaaaa	1639
aa						1641

<210> 353

<211> 884
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 69..557

<220>
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 <222> 69..224
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LGLALGRLEGGSA/RH

<220>
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 <222> 849..854

<220>
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 <222> 870..883

<220>
 <221> misc_feature
 <222> 623
 <223> n=a, g, c or t

<400> 353
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 caagcagg atg gag cac tac cgg aaa gct ggc tct gta gag ctc cca gcg 110
 Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
 -50 -45 -40
 cct tcc cca atg ccc cag cta cct cct gat acc ctt gag atg cgg gtc 158
 Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val
 -35 -30 -25
 cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct ctg ggt cgg 206
 Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
 -20 -15 -10
 ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt tct ggc agg 254
 Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
 -5 1 5 10
 gct gca gga aag gct gtc agc tgc gct gag att gtc aag cgg cgg gtc 302
 Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
 15 20 25
 ccg ggc ctg cac cag ctc acc aag cta ckt ttc ctt caa act gag gac 350
 Pro Gly Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp
 30 35 40
 agc tgg gtc cca scc tca cct gac aca ggg cta rac ccc ctc aca gtg 398
 Ser Trp Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val
 45 50 55
 cgc cgc cat gtg cct gca ktg tgg gtg ctg ctc asc cgg gac ccc ctg 446
 Arg Arg His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu
 60 65 70
 gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc cct ggc ctg 494
 Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu
 75 80 85 90

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ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cra aaa agg gct      542
Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala
          95                      100                      105
cra rac acc cga tcg tgaaaacctg ctgasccagc ctgttctccg ggcctraatg      597
Xaa Xaa Thr Arg Ser
          110
tctgggggtgc ttgtgccttt tctranaagc gttgtgaskg ctcaacatcc ccatcaagggt      657
ttgagtcacac aaaagtggac ctccctatca tgcttccctt tccctctagc atgtgggaag      717
ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt gctaaataag      777
ggcttctctt gccttctacc tacagtgcac ttgaactgcc ttctgaaaga ggtccakgga      837
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<210> 354
<211> 729
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 134..325

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<221> sig_peptide
<222> 134..274
<223> Von Heijne matrix
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      seq TWLGLLSFQNLHC/FP

<220>
<221> polyA_site
<222> 718..729

<400> 354
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tgtaatgcaa gtcccctaac tccctgggtg ctaacattaa cttccttaag taataatcaa      120
tgaaagavat tct atg cat ggt ttt gaa ata ata tcc ttg aaa gag gaa      169
      Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu
          -45                      -40
tca cca tta gga aag gtg agt cag ggt cct ttg ttt aat gtg act agt      217
Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser
-35                      -30                      -25                      -20
ggc tca tca tca cca gtg acc tgg ttg ggc cta ctc tcc ttc cag aac      265
Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn
          -15                      -10                      -5
ctg cat tgc ttc cca gac ctc ccc act gag atg cct cta ara gcc aaa      313
Leu His Cys Phe Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys
          1                      5                      10
gga ktc aac act tgagcctagg gtgggctaca acaaaaratt ctaatttacc      365
Gly Xaa Asn Thr
          15
ttgcttcacg taggtccagg ccccaaktg cttgctgaag gaacttaaaa agtagctggt      425
atattattgta ttgtataasc taaaaacatt tatttttgtt gaatcraaac aattccatgt      485
ascaatcttt tttctgttca cgggtgtttgt gataaaacct taaattccgc aagcatcagt      545
tttttgaaaa aatgggaatt gaccggatag wwacaggcaa agwtataaat agctacaaca      605
tcatttaact tttataaaca tgcttctctt ctattgaara catctgatat ttttgctgga      665
aagttggatc tatcctcagt aactctgcca tgaattcctg tttcckggtt ccaaaaaaaaa      725
aaaa      729

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<210> 355
 <211> 1013
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..731

<220>
 <221> sig_peptide
 <222> 78..227
 <223> Von Heijne matrix
 score 5.09999990463257
 seq RTALILAVCCGSA/SI

<220>
 <221> polyA_site
 <222> 1002..1013

<400> 355
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 aattttattt actttct atg cat cat ggc ctc aca cca ctg tta ctt ggt 110
 Met His His Gly Leu Thr Pro Leu Leu Leu Gly
 -50 -45 -40
 gta cat gag caa aaa cag caa gtg gtg aaa ttt tta atc aag aaa aaa 158
 Val His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys
 -35 -30 -25
 gca aat tta aat gca ctg gat aga tat gga aga act gct ctc ata ctt 206
 Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu
 -20 -15 -10
 gct gta tgt tgt gga tcg gca agt ata gtc agc ctt cta ctt gag caa 254
 Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
 -5 1 5
 aac att gat gta tct tct caa gat cta tct gga cag acg gcc aaa aag 302
 Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys
 10 15 20 25
 tat gct gtt tct agt cgt cat aat gta att tgc cag tta ctt tct gac 350
 Tyr Ala Val Ser Ser Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp
 30 35 40
 tac aaa raa aaa cag atr cta aaa gtc tct tct gaa aac agc aat cca 398
 Tyr Lys Xaa Lys Gln Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro
 45 50 55
 raa caa gac tta aag ctg aca tca gag gaa gag tca caa agg ctt aaa 446
 Xaa Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys
 60 65 70
 gga agt gaa aat agc cag cca gag gaa atg tct caa gaa cca gaa ata 494
 Gly Ser Glu Asn Ser Gln Pro Glu Glu Met Ser Gln Glu Pro Glu Ile
 75 80 85
 aat arg ggt ggt gat aga aag gtt gaa raa raa atg aar aag cac gga 542
 Asn Xaa Gly Gly Asp Arg Lys Val Glu Xaa Xaa Met Lys Lys His Gly
 90 95 100 105
 agt wct cat atg gga ttc cca raa aac ctg mct aac ggt gcc act gct 590
 Ser Xaa His Met Gly Phe Pro Xaa Asn Leu Xaa Asn Gly Ala Thr Ala
 110 115 120
 gac aat ggt gat gat gga tta att ccm cca rgg aaa asc ara aca cct 638

Asp Asn Gly Asp Asp Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro	
125 130 135	
gaa agc cas caa ttt cct gac act gag aat gaa cag tat cac agg gac	686
Glu Ser Xaa Gln Phe Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp	
140 145 150	
ttt tct ggc cat ccc mac ttt ccc acd acc ctt ccc atc aaa cag	731
Phe Ser Gly His Pro Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln	
155 160 165	
tgatgaacaa aatgatactc hsaagcmmct ttctgaagam caraacactg gaatattaca	791
agatgagatt ctgattcatg aagaaaagca gatagaagtg gctgaaaatg aattctgagc	851
tttctcttag ttataaaaa gaaaaagacc tcttgcatga aaatagtacg ttgcaggaag	911
aaattgtcat gctaaractg gaactagack taatgaaaca tcagagccag ctaaraaaa	971
araaatattt ggaggaaatt gaaagtgtgg aaaaaaaaaa aa	1013

<210> 356
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 46..693

<220>
 <221> sig_peptide
 <222> 46..90
 <223> Von Heijne matrix
 score 7.59999990463257
 seq CVLVLAAAAGAVA/VF

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 <222> 937..942

<220>
 <221> polyA_site
 <222> 962..973

<400> 356	
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Met Val Cys Val	
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ctc gtt cta gct gcg gcc gca gga gct gtg gcg gtt ttc cta atc ctg	105
Leu Val Leu Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu	
-10 -5 1 5	
cga ata tgg gta gtg ctt cgt tcc atg gac gtt acg ccc cgg gag tct	153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser	
10 15 20	
ctc agt atc ttg gta gtg gct ggg tcc ggt ggg cat acc act gag atc	201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile	
25 30 35	
ctg agg ctg ctt ggg agc ttg tcc aat gcc tac tca cct aga cat tat	249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr	
40 45 50	
gtc att gct gac act gat gaa atg agt gcc aat aaa ata aat tct ttt	297
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys Ile Asn Ser Phe	
55 60 65	

gaa cta rat cga gsk gat aga rac cct agt aac atg twt acc aaa tac	345
Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met Xaa Thr Lys Tyr	
70 75 80 85	
tac att cac cga att cca ara agc cgg gag gtt cag cag tcc tgg ccc	393
Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln Gln Ser Trp Pro	
90 95 100	
tcc acc gtt tyc acc acc ttg cac tcc atg tgg ctc tcc ttk ccc cta	441
Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu Ser Xaa Pro Leu	
105 110 115	
att cac agg gtg aag cca rat ttg gtg ttg tgt aac gga cca gga aca	489
Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn Gly Pro Gly Thr	
120 125 130	
tgt gty cct atc tgt gta tct gcc ctt ctc ctt ggg ata cta gga ata	537
Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly Ile Leu Gly Ile	
135 140 145	
aag aaa gtg atc att gtc tac gtt gaa agc atc tgc cgt gta aaa acs	585
Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys Arg Val Lys Thr	
150 155 160 165	
tta tcc atg tcc gga aag att ctg ttt cat ctc tca aat tac ttc att	633
Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser Asn Tyr Phe Ile	
170 175 180	
gtt cag tgg ccg gct ctg aaa gaa aag tat ccc aaa tcg gtg tac ctt	681
Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys Ser Val Tyr Leu	
185 190 195	
ggg cga att gtt tgacaaatgg caactgactt ctttagaatt ttgcasttaa	733
Gly Arg Ile Val	
200	
cagtartatg tactcaaatt ggggggaaaa aaaccctaca tgtttcttgt aaaggcgtct	793
gacagtcctg araattattg atggtaagga ataaaaaatg twcagatrac tcagtgaara	853
aactgaggct tctcttatga aacaaacatt gataaacgta actacyaaat gtttatgcct	913
ctgtaaacca aatttctttt ctarataaaa atatgtatta ctacctgcaa aaaaaaaaaa	973

<210> 357
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 126..527

<220>
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 <222> 126..182
 <223> Von Heijne matrix
 score 3.90000009536743
 seq ILFHGVFYAGGFA/IV

<220>
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 <222> 834..839

<220>
 <221> polyA_site
 <222> 856..867

<400> 357

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actggaagaa ctcgtcatgc tctttgtagc gtggtgcttc tgttgctcac aggacaactt      60
gcctttgatg attttcaaga gagttgtgct atgatgtggc aaagtatgca ggaagcaggc      120
ggtca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc      170
    Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
          -15                      -10                      -5
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg      218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
          1                      5                      10
act tta tat tac aag ttg gca gtg gar cag ctg car arc cat ccc gag      266
Thr Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu
          15                      20                      25
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc      314
Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
          30                      35                      40
atc gac agg gaa aac ttc gtg gac att gtt rat gcc aag ttg aaa att      362
Ile Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile
          45                      50                      55                      60
cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc      410
Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
          65                      70                      75
aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag      458
Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
          80                      85                      90
ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac      506
Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
          95                      100                      105
ggt gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt      557
Gly Asp Glu Val Lys Lys Glu
          110                      115
ctagtccatc cttccctcat ctctaccata tggccactgg ggtggtggcc catctcagtg      617
acagacactc ctgcaaccca gktttcagc caccagtggg atgatggtat gtgccagcac      677
atggtaattt tgggtgtaatt ctaacttggg cacaacgaat gctatttgtc atttttaaac      737
tgaatccgaa agaaactcct attataaatt taagataatg taatgtattt gaaagtgcctt      797
tgtataaaaa agcacatgat aaaaggaatc agaattaata aaatgtttgt tgatctttaa      857
aaaaaaaaaa h                                                                868

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<210> 358
 <211> 519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..320

<220>
 <221> sig_peptide
 <222> 66..113
 <223> Von Heijne matrix
 score 3.5
 seq TALAAXTWLGVWG/VR

<220>
 <221> polyA_signal
 <222> 490..495

<220>

<221> polyA_site

<222> 508..519

<400> 358

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aattagcgcg taacgcasag actgcttgct gcggcagaga cgccagakgt gcagctccag      60
cagca atg gca gtg acg gcg ttg gcg gcg mrg acg tgg ctt ggc gtg tgg      110
      Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
      -15              -10              -5
ggc gtg agg acc atg caa gcc cga ggc ttc ggc tcg gat cag tcc gag      158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
      1              5              10              15
aat gtc gac cgg ggc gcg ggc tcc atc cgg gaa gcc ggt ggg gcc ttc      206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
      20              25              30
gga aag aga gag cag gct gaa gag gaa cga tat ttc cga gca cag agt      254
Gly Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser
      35              40              45
aca gaa caa ctg gca rct ttg aaa aaa crc cat gaa gaa gar atc gtt      302
Thr Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val
      50              55              60
cat cat aga gaa gga gat tgagcgtctg cagaaagaaa ttgagcgcca      350
His His Arg Glu Gly Asp
      65
taagcagaag atcaaaatgc tagaacatga tgattaagtg cacaccgtgt gccatagaat      410
ggcacatgtc attgccact tctgtgtaaa catgggttctg gtttaactaa tatttgtctg      470
tgtgtacta acagattata ataaattgtc atcagtgaaa aaaaaaaaaa      519
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<210> 359

<211> 1028

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 73..948

<220>

<221> sig_peptide

<222> 73..159

<223> Von Heijne matrix

score 4.40000009536743

seq IVLHLVLQGMVYT/EY

<220>

<221> polyA_site

<222> 1016..1028

<400> 359

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agctttaaag gcctggccag gggaggagca cagatatttt cctgtataat tccagaatgt      60
cttcagagag cc atg cat gga ttg ctt cat tac ctt ttc cat acg aga aac      111
      Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn
      -25              -20
cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act      159
His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr
      -15              -10              -5
gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc      207
Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser
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1	5	10	15	
ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt				255
Leu His Tyr	Leu Leu Pro Tyr	Leu Leu Gly Val	Asn Leu Phe	
20	25	30		
ttt ttc acc ctg act tgt gga acc aat cct ggc att ata aca aaa gca				303
Phe Phe Thr	Leu Thr Cys Gly Thr	Asn Pro Gly Ile	Ile Thr Lys Ala	
35	40	45		
aat gaa tta tta ttt ctt cat gtt tat gaa ttt gat gaa ktg atg ttt				351
Asn Glu Leu Leu Phe	Leu His Val Tyr Glu Phe	Asp Glu Xaa Met	Phe	
50	55	60		
cca aaa aac gtg agg tgc tct act tgt gat tta agg aaa cca gct cga				399
Pro Lys Asn Val Arg	Cys Ser Thr Cys Asp	Leu Arg Lys Pro	Ala Arg	
65	70	75	80	
tcc aas cac tgc akt gtg tgt aac tgg tgt gtg cac cgt ttc rac cat				447
Ser Xaa His Cys	Xaa Val Cys Asn Trp	Cys Val His Arg	Phe Xaa His	
85	90	95		
cac tgt gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc agg tmc				495
His Cys Val Trp	Val Asn Asn Cys Ile	Gly Ala Trp Asn	Ile Arg Xaa	
100	105	110		
ttc ctc atc tac gtc ttg acc ttg acg gcc tcg gct gcc acc gtc gcc				543
Phe Leu Ile Tyr	Val Leu Thr Leu Thr	Ala Ser Ala Ala	Thr Val Ala	
115	120	125		
att gtg agc acc act ttt ctg gtc cac ttg gtg gtg atg tca gat tta				591
Ile Val Ser Thr Thr	Phe Leu Val His Leu Val	Val Met Ser Asp	Leu	
130	135	140		
tac cag gag act tac atc gat gac ctt gga cac ctc cat gtt atg gac				639
Tyr Gln Glu Thr Tyr	Ile Asp Asp Leu Gly	His Leu His Val	Met Asp	
145	150	155	160	
acg gtc ttt ctt att cag tac ctg ttc ctg act ttt cca cgg att gtc				687
Thr Val Phe Leu Ile	Gln Tyr Leu Phe Leu Thr	Phe Pro Arg Ile	Val	
165	170	175		
ttc atg ctg ggc ttt gtc gtg gtt ctg arc ttc ctc ctg ggt ggc tac				735
Phe Met Leu Gly	Phe Val Val Val Leu Xaa	Phe Leu Leu Gly	Gly Tyr	
180	185	190		
ctg ttg ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac gag				783
Leu Leu Phe Val Leu Tyr	Leu Ala Ala Thr Asn	Gln Thr Thr Asn	Glu	
195	200	205		
tgg tac aga rgt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg gcc				831
Trp Tyr Arg Xaa Asp	Trp Ala Trp Cys Gln Arg	Cys Pro Leu Val	Ala	
210	215	220		
tgg cct ccg tca gca gar ccc caa gtc cac cgg aac att cac tcc cat				879
Trp Pro Pro Ser Ala	Glu Pro Gln Val His Arg	Asn Ile His Ser	His	
225	230	235	240	
ggg ctt cgg arc aac ctt caa gar atc ttt cta cct gcc ttt cca tgt				927
Gly Leu Arg Xaa Asn	Leu Gln Glu Ile Phe Leu	Pro Ala Phe Pro	Cys	
245	250	255		
cat gag agg aag aaa caa gaa tgacmagtgt atgactgcct ttgagctgta				978
His Glu Arg Lys Lys	Gln Glu			
260				
gttcccgttt atttacacat gtggatcctc gttttccaaa aaaaaaaaaa				1028

<210> 360
 <211> 452
 <212> DNA
 <213> Homo sapiens
 <220>

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<221> CDS
<222> 69..434

<220>
<221> sig_peptide
<222> 69..236
<223> Von Heijne matrix
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      seq FACVPGASPTTLA/FP

<220>
<221> polyA_signal
<222> 419..424

<220>
<221> polyA_site
<222> 441..452

<220>
<221> misc_feature
<222> 45,291
<223> n=a, g, c or t

<400> 360
acagcgtgas tcgcccgcc gaagaatatg aaaaagcaga gcganctcgg ttaagggaaa      60
gcgccgag atg acg ggc ttt ctg ctg ccg ccc gca agc aga ggg act cgg      110
      Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg
            -55                    -50                    -45
aga tca tgc agc aga agc aga aaa agg caa acg aga aga agg agg aac      158
Arg Ser Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn
      -40                    -35                    -30
cca agt agc ttt gtg gct tcg tgt cca acc ctc ttg ccc ttc gcc tgt      206
Pro Ser Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys
      -25                    -20                    -15
gtg cct gga gcc agt ccc acc acg ctc gcg ttt cct cct gta ktg ctc      254
Val Pro Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu
      -10                    -5                    1                    5
aca ggt ccc avc acc gat ggc att ccc ttt gcc ctr nak tct gca gcg      302
Thr Gly Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala
            10                    15                    20
ggg ccc ttt tgt gct tcc ttc ccc tca ggt avc ctc tct ccc cct ggg      350
Gly Pro Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly
            25                    30                    35
cca ctc ccg ggg gtg agg ggg tta ccc ctt ccc agt gtt ttt tat tcc      398
Pro Leu Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser
      40                    45                    50
tgt ggg gct cac ccc aaa gta tta aaa gta gct ttg taattcaaaa      444
Cys Gly Ala His Pro Lys Val Leu Lys Val Ala Leu
55                    60                    65
aaaaaaaaa      452

<210> 361
<211> 875
<212> DNA
<213> Homo sapiens

<220>

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<221> CDS
<222> 628..804

<220>
<221> sig_peptide
<222> 628..711
<223> Von Heijne matrix
      score 4.19999980926514
      seq LMPVIPALQEAXA/GG

<220>
<221> polyA_site
<222> 864..875

<220>
<221> misc_feature
<222> 106,708
<223> n=a, g, c or t

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gaaaccgctt tatcatcctt gtgtatgtac tggcagtatt aagttngtcc atcaagaatg      120
cttagttcaa tggctgaaac acagtcgaaa agaatactgt gaattatgca agcacagatt      180
tgcttttaca ccaatttatt ctccagatat gccttcacgg cttccaattc aagacatatt      240
tgctggactg gttacaagta ttggcactgc aatacgatat tggtttcatt atacacttgt      300
ggcctttgca tggttgggag ttgttcctct tacagcatgt gagtattcat gcctctgatt      360
ggagtatttt aaacattgca taactactta atattataaa gcaatattgc atcataattat      420
tatttgactg atgttttagtt atttgatgtc agagtgtcat gtattaggaa agccttactt      480
araaratgtt catcggaact aaraatgakt ttaacaggtc agttttttga gtgaatgtgg      540
gaaaraacac agcatacaga atggctaacc atgaaagtcc atgaaagcgt kgaaaaaatc      600
aatcaaatac ataattagat atgaagt atg cta rag ctt tca agg gct aca aaa      654
                               Met Leu Xaa Leu Ser Arg Ala Thr Lys
                               -25                               -20

rac ggc cgg gcg cgg tgg ctt atg cct gta atc cca gca ctt cag gag      702
Xaa Gly Arg Ala Arg Trp Leu Met Pro Val Ile Pro Ala Leu Gln Glu
                               -15                               -10                               -5

gcc gan gca ggc gga tca cga ggt cag gag ttt gaa act agc ctg gcc      750
Ala Xaa Ala Gly Gly Ser Arg Gly Gln Glu Phe Glu Thr Ser Leu Ala
                               1                               5                               10

aac atg gag act gag gca gga gaa ttg ctt aaa ccc agg agg cgg agg      798
Asn Met Glu Thr Glu Ala Gly Glu Leu Leu Lys Pro Arg Arg Arg Arg
                               15                               20                               25

ttg car tgaactgaga tcgcaccact gcactccagc ttgggcaaca gagcaagact      854
Leu Gln
30
ttgtctcgca aaaaaaaaaa a      875

<210> 362
<211> 531
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..366

<220>

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<221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLLSNWANPASS/RR

<220>
 <221> polyA_signal
 <222> 496..501

<220>
 <221> polyA_site
 <222> 521..531

<400> 362
 aagtggccat ggcggataca gcgactacag catcggcggc ggcggctagt gccgctagcg 60
 cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga 111
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
 -10 -5 1
 cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc 159
 Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
 5 10 15
 gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc 207
 Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
 20 25 30
 tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac 255
 Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
 35 40 45
 agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca 303
 Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
 50 55 60 65
 cca atg aga aga tct tca tgc cat tta gaa tgt crg gtt ata ttc ctt 351
 Pro Met Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu
 70 75 80
 ttg gga cgc caa ttg taaktgttac cttcaaagga tttccttttc taaaaaatta 406
 Leu Gly Arg Gln Leu
 85
 ttttaratgt ctaactttat gttattgctc acgggtatgt gactgaattg ttgatttagg 466
 ataagtcaat tcctggaggg aaattaccaa ataaaatgat atgtatttct taccacaaaa 526
 aaaaa 531

<210> 363
 <211> 1244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..366

<220>
 <221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLLSNWANPASS/RR

<220>
 <221> polyA_site
 <222> 1233..1244

<400> 363
 aagtggccat ggcggataca gcgactacag catcggcggc ggcggctagt gccgctagcg 60
 cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga 111
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
 -10 -5 1
 cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc 159
 Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
 5 10 15
 gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc 207
 Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
 20 25 30
 tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac 255
 Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
 35 40 45
 agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca 303
 Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
 50 55 60 65
 cca atg aga aga tct tca tgc cat tta raa tgt cag gtt ata ttc ctt 351
 Pro Met Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu
 70 75 80
 ttg gga cgc caa ttg tagtcggtct tctcttgccc aaccagacac tggcatccac 406
 Leu Gly Arg Gln Leu
 85
 tgtcttcttg cagtggctga accagagcca caatgcctgt gtcaactatg caaaccgcaa 466
 tgraccaag ccttcacctg catccaagtt catccaggga tacctgggag ctgtcatcag 526
 cgccgtctcc attgctgtgg gccttatktc ctgggtcaga aagccaacaa gttcacccca 586
 gccaccgccc ttctcatcca gaggtttgtg ccgttcctct ctgtagccag tgccaatata 646
 tgcaatgtgg tctgatgctg gtacggggag ctggaggaag ggattgatgt cctggacagc 706
 gatggcaacc tcgtgggctc ctccaagatc gcagcccgc acgccctgct ggagacggcg 766
 ctgacgcgag tggctcctgc catgcccata ctggtgctac ccccgatcgt catgtccatg 826
 ctggagaaga cggctctcct gcaggcacgc ccccggtgc tctcctctgt gcaaagcctc 886
 gtgtgccttg cagccttcgg cctggccctg ccgctggcca tcagcctctt cccgcaaata 946
 tcagagattg aaacatccca attagagccg gagatagccc aggccacgag cagccggaca 1006
 gtggtgtaca acaaggggtt gtgagtgtgg tcagcggcct ggggacggag cactgtgcag 1066
 ccggggagct gaggggcarg gccgtagact cacggctgca cctgcaggga gcagcacgcc 1126
 aaccccagca gtcttgggcc cctggggaga gtgctcaacc tacagtggag ggagactgac 1186
 ccattcacat tttaacatag gcaagaggag ttctaacaca tttcgtacaa aaaaaaaa 1244

<210> 364
 <211> 631
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 111..434

<220>
 <221> sig_peptide
 <222> 111..185
 <223> Von Heijne matrix
 score 3.90000009536743
 seq WIAAVTIAAGTAA/IG

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<220>
<221> polyA_site
<222> 618..631

<400> 364
aatcgcgaggag tcggtgcttt agtacgccgc tggcaccttt actctcgccg gccgcgcgaa      60
cccgtttgag ctcggtatcc tagtgacacac gccttgcaag cgacggcgcc atg agt      116
                                   Met Ser
                                   -25
ctg act tcc agt tcc agc gta cga gtt gaa tgg atc gca gca gtt acc      164
Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
                                   -20      -15      -10
att gct gct ggg aca gct gca att ggt tat cta gct tac aaa aga ttt      212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
                                   -5      1      5
tat gtt aaa gat cat cga aat aaa gct atg ata aac ctt cac atc cag      260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
10      15      20      25
aaa gac aac ccc aag ata gta cat gct ttt gac atg gag gat ttg gga      308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly
                                   30      35      40
gat aaa gct gtg tac tgc cgt tgt tgg agg tcc aaa aag ttc cca ttc      356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
                                   45      50      55
tgt gat ggg gct cac aca aaa cat aac gaa gag act gga gac aat gtg      404
Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val
60      65      70
ggc cct ctg atc atc aag aaa aaa gaa act taaatggaca cttttgatgc      454
Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
75      80
tgcaaatcag cttgtcgtga agttacctga ttgtttaatt araatgacta ccacctctgt      514
ctgattcacc ttcgctggat tctaaatgtg gtatattgcm aactgcagct ttcacattta      574
tggcatttgt cttgttgaaa catcgtggtg cacatttgtt taaacaaaaa aaaaaaa      631

<210> 365
<211> 781
<212> DNA
<213> Homo sapiens

<220>
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<222> 19..567

<220>
<221> sig_peptide
<222> 19..63
<223> Von Heijne matrix
      score 8.39999961853027
      seq AMWLLCVALAVLA/WG

<220>
<221> polyA_signal
<222> 749..754

<220>
<221> polyA_site

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<222> 771..781

<400> 365

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aagtgtgtgct tacccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      51
                        Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                        -15                      -10                      -5

gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
                        1                      5                      10

atg aag agt cgg gag cag gga aga cgg ctg gga gcc gaa agc cgg acc      147
Met Lys Ser Arg Glu Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr
                        15                      20                      25

ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc      195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
                        30                      35                      40

aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45                      50                      55                      60

ttc tct gca gga aat tac tac aat caa gga gag act cgt aag aaa gaa      291
Phe Ser Ala Gly Asn Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu
                        65                      70                      75

ctt ttg car agc tgt gat gtt ttg ggg att cca ctc tcc agt gta atg      339
Leu Leu Gln Ser Cys Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met
                        80                      85                      90

att att gac aac agg gat ttc cca rat gac cca ggc atg cag tgg gac      387
Ile Ile Asp Asn Arg Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp
                        95                      100                      105

aca rag cac gtg gcc ara gtc ctc ctt cag cac ata gaa gtg aat ggc      435
Thr Xaa His Val Ala Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly
110                      115                      120

atc aat ctg gtg gtg act ttc gat gca ggg gga rta agt ggc cac agc      483
Ile Asn Leu Val Val Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser
125                      130                      135                      140

aat cac att gct ctg tat gca gct gtg agg aag ctt gag ggc caa att      531
Asn His Ile Ala Leu Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile
                        145                      150                      155

tgc aag ccc tgt ggc act gga caa gac ttt aag gaa tgagtgtgt      577
Cys Lys Pro Cys Gly Thr Gly Gln Asp Phe Lys Glu
                        160                      165

caatcagtgt gctccacct tcaccatctt cttcccttta ctctcacttc cgtcatgtgt      637
tttatacaac tctcaaatct ttcttggaga aggaggatat acatacataa tatgaaatgt      697
gtttgtttctt cacagtcacc cgattttact gatattttatt tgcattttac caataaaaag      757
aaaatgcaag ctcaaaaaaa aaaa      781
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<210> 366

<211> 931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 19..312

<220>

<221> sig_peptide

<222> 19..63

<223> Von Heijne matrix

score 8.39999961853027
seq AMWLLCVALAVLA/WG

<220>
<221> polyA_signal
<222> 896..901

<220>
<221> polyA_site
<222> 921..931

<220>
<221> misc_feature
<222> 388,391
<223> n=a, g, c or t

<400> 366
aagtgtctgct tacccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg 51
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
-15 -10 -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga 99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
1 5 10
atg aag agt cgg gag cag gga rga cgg ctg gga gcc gaa agc cgg acc 147
Met Lys Ser Arg Glu Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr
15 20 25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc 195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
30 35 40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc 243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45 50 55 60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa rgt ctt 291
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu
65 70 75
acc tct gaa ccc ctc ama gcc tagggacagg arcggccggc ttacctggtg 342
Thr Ser Glu Pro Leu Xaa Ala
80
ggttggggga cgtcggcagc tcrctgacta cgccagcagg attganganc acagaaacag 402
ttgchsttgg ttgtattcag tacctkcatt tccgttggga actccaccwg tacttggtat 462
kctgtggaac ttttttttat ttgtagaagg agcaagaata ttgaccttac tatatagcac 522
acgaaacaat ctatgctgta tcgtgcctgc tcaatcctta aagttaactt ctaatgatag 582
taaaaracct tcctgctgcc tttaaaatgc agcttgtgct aktaacatgc atgtgtcaaa 642
ttgaaraatt agacatagat gactaratar aaagtaattt ttaggtaat tttaragttc 702
aactccaccc agctttcakt gaaggaacct ttcaaataat aratttttgc ttaccatara 762
raaaaratca aatgacaaag caaatattga ccattaagct ggaatatggt gataattgaa 822
cagttgtata aatgaaktaa ttgaattgta cacatacaat gggtgaattt tatggcatgt 882
caaagtatac ctcaataaag ctattttttt aaattgcmaa aaaaaaaaaa 931

<210> 367
<211> 849
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 64..612

<220>
 <221> sig_peptide
 <222> 64..234
 <223> Von Heijne matrix
 score 3.79999995231628
 seq QLWLVMEFCGAGS/VT

<220>
 <221> polyA_site
 <222> 839..849

<400> 367
 acatacgggc aagtttataa gggtcgtcat gtcaaaacgg gccagcttgc agccatcaag 60
 gtt atg gat gtc aca ggg gat gaa gag gaa gaa atc aaa caa gaa att 108
 Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile
 -55 -50 -45
 aac atg ttg aag aaa tat tct cat cac cgg aat att gct aca tac tat 156
 Asn Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr
 -40 -35 -30
 ggt gct ttt atc aaa aag aac cca cca ggc atg gat gac caa ctt tgg 204
 Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp
 -25 -20 -15
 ttg gtg atg gag ttt tgt ggt gct ggc tct gtc acc gac ctg atc aag 252
 Leu Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys
 -10 -5 1 5
 aac aca aaa ggt aac acg ttg aaa gag gag tgg att gca tac atc tgc 300
 Asn Thr Lys Gly Asn Thr Leu Lys Glu Glu Trp Ile Ala Tyr Ile Cys
 10 15 20
 msg gaa atc tta cgg ggg ctg art cac ctg cac cag cat aaa gtg att 348
 Xaa Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile
 25 30 35
 cat cga rat att aaa ggg caa aat gtc ttg ctg act gaa aat gca gaa 396
 His Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu
 40 45 50
 gtt aaa cta gtg gac ttt gga rtc akt gct cag ctt gat cga aca gtg 444
 Val Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val
 55 60 65 70
 ggc agg arg aat act ttc att gga act ccc tac tgg atg gca cca raa 492
 Gly Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa
 75 80 85
 gtt att gcc tgt gat gaa aac cca sat gcc aca tat gat ttc aar art 540
 Val Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa
 90 95 100
 gac ttg tgg tct ttg ggt atc acc gcc att gaa atg gca gaa ggg ctc 588
 Asp Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu
 105 110 115
 ccc ctc tct gtg aca tgc acc cca tgagagctct cttcctcatc ccccggaatc 642
 Pro Leu Ser Val Thr Cys Thr Pro
 120 125
 cagcgcctcg gctgaagtct aagaagtggc caaaaaaatt ccagtcattt attgagagct 702
 gcttggtaaa aaatcacagc cagcgaccag caacagaaca attgatgaag catccattta 762
 tacgagacca acctaatgag cgacaggtcc gcattcaact caaggaccat attgatagaa 822
 caaagaagaa gcgaggaaaa aaaaaaa 849

<210> 368
 <211> 644

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..458

<220>
<221> sig_peptide
<222> 39..80
<223> Von Heijne matrix
score 4.40000009536743
seq FLTALLWRGRIPG/RQ

<220>
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<222> 613..618

<220>
<221> polyA_site
<222> 633..644

<220>
<221> misc_feature
<222> 30
<223> n=a, g, c or t

<400> 368
agcggagacg cagagtcttg agcagcgcggn caggcacc atg ttc ctg act gcg ctc 56
Met Phe Leu Thr Ala Leu
-10
ctc tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg 104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg
-5 1 5
cgg ccg cgg ttc gtg tgg cgc gcc aag cag aac atg atc cgc cgc 152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg
10 15 20
ctg gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg 200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met
25 30 35 40
acc cgg gag cag gag cgc gcc cac gcc gcg ttg cgc agg agg gag gcc 248
Thr Arg Glu Gln Glu Arg Gly His Ala Ala Leu Arg Arg Arg Glu Ala
45 50 55
ttc gag gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga 296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg
60 65 70
ttc att gcg gac cag ctc gac cat ctc aat vgt cac caa gaa atg gtc 344
Phe Ile Ala Asp Gln Leu Asp His Leu Asn Xaa His Gln Glu Met Val
75 80 85
cta atc ctg agt cgt cac cct tgg att tta tgg atc acg gag ctg acc 392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr
90 95 100
atc ttt acc tgg tct gga ctg aaa aac tgt agc ttg tgt gaa aat gag 440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu
105 110 115 120
ctt tgg acc agt ctt tat taaaacaaac aaacatgagt agtctgcata 488
Leu Trp Thr Ser Leu Tyr

125
tcgaatatct agagctctaa acccccctaat acttaaaagt ctaattgctg tectgtgggt 548
tcattagtct gataggaaga tagggatttc ctcagtcaca gatgatattt tgaaggaaag 608
ctgcaataaa gccacaatga ttgaaaaaa aaaaaa 644

<210> 369
<211> 918
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..185

<220>
<221> sig_peptide
<222> 9..50
<223> Von Heijne matrix
score 3.70000004768372
seq AALVTVLFTGVRR/LH

<220>
<221> polyA_site
<222> 906..918

<400> 369
agctcagc atg gct gct tta gtg act gtt ctc ttc aca ggt gtc cgg agg 50
Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg
-10 -5
ctg cac tgc agc gcr scg ctt ggg cgg gcg gcc agt ggc grc tac agc 98
Leu His Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser
1 5 10 15
agg aac tgg ctg cca acc cct ccg gct acg ggc ccc tta ccg agc tcc 146
Arg Asn Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser
20 25 30
cag act ggt cat atg cgg atg gcc gcc ctg ctc ccc caa tgaaaggcca 195
Gln Thr Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
35 40 45
gcttcgaaaa aaagctgaaa gggagacktt tgcaaracra kttgtactgc tgtcacagga 255
aatggacgct ggattacaas catggcasct caggcagcar aakttgagg aaraacaaag 315
gaagcaggaa aatgctctta aacccaaagg ggcttcactg aaaascccac ttccaaktca 375
ataaaaaagca actcctgcct cccttcctca ccctgtctct ggattttctt tctatcacct 435
aratgcttca tccagccara aaatagcctt cackktcccc atctgtcttc aragcaaaar 495
agctgggacm ccaaraacaa gctgttarat cactgcctgg gaggcttggc ttartactct 555
catctctggg tccattccag ttcagctaag tcttgcttta aaatttttac ctctagctg 615
gggtgcgggtg ctacgcctg taatcccagc actttgggag gctgaggcgg gcagatcaca 675
agatcaggag ttcgagacca gcctggccaa cccagcctgg tcaacatggg gaaaccctgt 735
ccctactaaa gatacaaaca attagccggg cgtgggtggg tgcgcttgta atcccagcta 795
ctcaggaggc tgaggcagga gaatcgctta aactcgggag gtagagggtg cagtgagcca 855
aggtcacacc attgcactcc aacctgggag acagggcgag actctgtctc aaaaaaaaaa 915
aaa 918

<210> 370
<211> 472
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 14..316

<220>
 <221> sig_peptide
 <222> 14..121
 <223> Von Heijne matrix
 score 5.19999980926514
 seq PLRLNLLILIEG/SV

<220>
 <221> polyA_signal
 <222> 442..447

<220>
 <221> polyA_site
 <222> 458..471

<400> 370
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 Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val
 -35 -30 -25
 tct cat gcc cgc ttt tat ttc tta ttt cat cga cca tta agg ctg tta 97
 Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu
 -20 -15 -10
 aat ctg ctc atc ctt att gag ggc agt gtc gtc ttc tat cag ctc tat 145
 Asn Leu Leu Ile Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr
 -5 1 5
 tcc ttg ctg cgg tcg gag aag tgg aac cac aca ctt tcc atg gct ctc 193
 Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu
 10 15 20
 atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt ctc cgg gac aga 241
 Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg
 25 30 35 40
 wta kta tta ggc agg gca tac tcc tac cca ctc aac agt tat gaa ctc 289
 Xaa Xaa Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu
 45 50 55
 aag gca aac twa gct gcc tct caw caa tgagggagaa ctcagataaa 336
 Lys Ala Asn Xaa Ala Ala Ser Xaa Gln
 60 65
 aatattttca tacgttctat ttttttcttg tgatttttat aaatatttaa gatattttat 396
 attttgtata ctattatgtt ttgaaagtcg ggaagagtaa gggatattaa atgtatccgt 456
 aaacaaaaaa aaaaam 472

<210> 371
 <211> 1504
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 70..1092

<220>
 <221> sig_peptide
 <222> 70..234

<223> Von Heijne matrix
 score 4.09999990463257
 seq AVCAALLASHPTA/EV

<220>

<221> polyA_signal

<222> 1475..1480

<220>

<221> polyA_site

<222> 1493..1504

<400> 371

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tgcgcgaag atg cga aag gtg gtt ttr att acc ggg gct agc agt ggc att      111
      Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile
      -55              -50              -45
ggc ctg gcc ctg tgc aag cgg ctg ctg gcg gaa gat gat gag ctt cat      159
Gly Leu Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His
      -40              -35              -30
ctg tgt ttg gcg tgc agg aat atg agc aag gca gaa gct gtc tgt gct      207
Leu Cys Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala
      -25              -20              -15              -10
gct ctg ctg gcc tct cac ccc act gct gag gtc acc att gtc cag gtg      255
Ala Leu Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val
      -5              1              5
gat gtc agc aac ctg cag tca ttc ttc cgg gcc tcc aag gaa ctt aag      303
Asp Val Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys
      10              15              20
caa agg ttt cag aga tta gac tgt ata tat cta aat gct ggg atc atg      351
Gln Arg Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met
      25              30              35
cct aat cca caa cta aat atc aaa gca ctt ttc ttt ggc ctg ttt tca      399
Pro Asn Pro Gln Leu Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser
      40              45              50              55
aga aaa gtg att cat atg ttc tcc aca gct gaa ggc ctg ctg acc cag      447
Arg Lys Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln
      60              65              70
ggg gat aag atc act gct gat gga ctt cag gag gtg ttt gag acc aat      495
Gly Asp Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn
      75              80              85
gtc ttt ggc cat ttt atc ctg att cgg gaa ctg gag cct ctg ctg tgt      543
Val Phe Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys
      90              95              100
cac agt gac aat cca tct cag ctg atc tgg aca tca tct cgc agt gca      591
His Ser Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala
      105              110              115
agg aaa tct aat ttc agc ctg gag gac ttc cag cac agc aaa ggc aag      639
Arg Lys Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys
      120              125              130              135
gaa ccc tac agc tct tcc aaa tat gcc act gac ctt ttg agt gtg gct      687
Glu Pro Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala
      140              145              150
ttg aac agg aac ttc aac cag cag ggt ctg tat tcc aat gtg gcc tgt      735
Leu Asn Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys
      155              160              165
cca ggt aca gca ttg acc aat ttg aca tat gga att ctg cct ccg ttt      783

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Pro Gly Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe	
170 175 180	
ata tgg acg ctg ttg atg ccg gca ata ttg cta ctt cgc ttt ttt gca	831
Ile Trp Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala	
185 190 195	
aat gca ttc act ttg aca cca tat aat gga aca gaa gct ctg gta tgg	879
Asn Ala Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp	
200 205 210 215	
ctt ttc cac caa aag cct gaa tct ctc aat cct ctg atc aaa tat ctg	927
Leu Phe His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu	
220 225 230	
agt gcc acc act ggc ttt gga aga aat tac att atg acc cag aag atg	975
Ser Ala Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met	
235 240 245	
gac cta gat gaa gac act gct gaa aaa ttt tat caa aag tta ctg gaa	1023
Asp Leu Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu	
250 255 260	
ctg gaa aag cac att agg gtc act att caa aaa aca gat aat cag gcc	1071
Leu Glu Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala	
265 270 275	
agg ctc agt ggc tca tgc cta taattccagc actttgggag gccaaaggcag	1122
Arg Leu Ser Gly Ser Cys Leu	
280 285	
aaggatcact tgagaccagg agttcaagac cagcctgaga aacatagtgga gcccttgtct	1182
ctacaaaaag aaataaaaat aatagctggg tgtggtggca tgcgcatgta gtcccagcta	1242
ctcagaagga tgaggtggga ggatctcttg aggctgggag gcagaggttg cagtgagctg	1302
agattgtgcc actgcactcc agcctgggtg acagcgagac cctgtctcaa aatatgtata	1362
tatttaatat atatataaaa ccagagctga caatgacact ctggaacatt gcataccttc	1422
tgtacattct ggggtacatg gatttctact gagttggata atatgcattt gtaataaact	1482
atgaactatg aaaaaaaaaa aa	1504

<210> 372
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 274..597

<220>
 <221> sig_peptide
 <222> 274..399
 <223> Von Heijne matrix
 score 5.19999980926514
 seq LLFDLVCHEFCQS/DD

<220>
 <221> polyA_signal
 <222> 731..736

<220>
 <221> polyA_site
 <222> 754..765

<220>
 <221> misc_feature

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<222> 552
<223> n=a, g, c or t

<400> 372
accaggaaca tccagctatt tatgatagca tttgcttcat tatgtcaagt tcaacaaatg      60
ttgacttgct ggtgaagggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac      120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag      180
tctgaagagc agccagtgtt tcggcttctg cctgtatac ttgaagctgc caaacaagta      240
cgttctgaaa atccagaatg gcttgatgtt tac atg cac att tta caa ctg ctt      294
                               Met His Ile Leu Gln Leu Leu
                               -40

act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act      342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35                               -30                               -25                               -20
gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc      390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
                               -15                               -10                               -5
tgc cag tct gat gat cca gcc atc att ctt caa raa car aaa acr gtg      438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Xaa Gln Lys Thr Val
                               1                               5                               10
cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act      486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
15                               20                               25
gag caa gak tat cta aar ata raa aaa gga gac ggt ggc tca ggg agt      534
Glu Gln Xaa Tyr Leu Lys Ile Xaa Lys Gly Asp Gly Gly Ser Gly Ser
30                               35                               40                               45
aaa gga agg cca ktt gan caa aca gaa ktg ttc ctc tgc att tca aaa      582
Lys Gly Arg Pro Xaa Xaa Gln Thr Glu Xaa Phe Leu Cys Ile Ser Lys
                               50                               55                               60
cct tct tcc ttt cta tagccctgtg gtggaagatt ttattaaaat cctacgtgaa      637
Pro Ser Ser Phe Leu
65
gttgataagg cgcttgctga tgacttgga aaaaacttcc caagtttgaa ggttcagact      697
taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa      757
aaaaaaaaa                                                                765

<210> 373
<211> 1041
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 230..469

<220>
<221> sig_peptide
<222> 230..307
<223> Von Heijne matrix
      score 4.90000009536743
      seq VLCTNQVLITARA/VP

<220>
<221> polyA_signal
<222> 1004..1009

<220>

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<221> polyA_site

<222> 1027..1040

<400> 373

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aacttccaag ttgtagtggt gttgttttca gcctgctgct gctgctgcta ttgcgggctag    60
gggaaccgtc gtggggaagg atggtgtgcg aaaaatgtga aaagaaactt ggtactgtta    120
tcactccaga tacatggaaa gatggtgcta ggaataccac agaaagtggg ggaagaaagc    180
tgaatgaaaa taaagctttg acttcaaaaa aagccagaat tgatccata atg gaa gaa    238
                                   Met Glu Glu
                                   -25
ata agt tct cca ctt gta gaa ttt gta aaa gtt ttg tgc acc aac cag    286
Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
                                   -20      -15      -10
gtt ctc att act gcc agg gct gtg cct aca aaa aag gca tct gtg cga    334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
                                   -5      1      5
tgt gtg gaa aaa agg ttt tgg ata cca aaa act aca agc aaa cat ctg    382
Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
10      15      20      25
tct aga tgt att gat gga att tct ggc ttt cta aat gat ttt act ttc    430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
                                   30      35      40
tgc ctt gaa ttt tca agg cat aga tgt caa ctt aca gaa taacatgkt    479
Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
                                   45      50
taagataatt aagtktaaac cagaraatth gattgttact cattttgctc tcatgtkcta    539
aaacagcaac agtgtaacta gtcttttggt gtaaatgggt attttcctta taaaaattht    599
aaaaactaag tggcaaattc catgaaaata tttctcagtt ctgtatgcac ttttatttaa    659
cattattcat ataattctcc cccaccact ttatttataa atactgcaaa aktgaraagg    719
agataataaa tactttgctc tgaatttggc atccaaagtt aacattttctc cctcactcc    779
cttgctgggtg tcatagttat tagaatcagc agcctcttaa ctaattgcgg tttcatagga    839
tatataaatg tttcaagcca ttattgctga atggttcttt agttattaac ctagacccaa    899
atcaaagacc agttggattt atgatatttt ttatttggtc ttgcagccaa agtgccagtt    959
tctttaatat gtgaccaaga acacaaggag catccatatt gccaaataaa tacactgaat   1019
tttagaaaaa caaaaaaaaa ar                                           1041
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<210> 374

<211> 1164

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 72..545

<220>

<221> sig_peptide

<222> 72..203

<223> Von Heijne matrix

score 5.5

seq ILFTGWWIMIDA/AV

<220>

<221> polyA_site

<222> 1151..1162

<400> 374

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aaagtcggcg tggacgtttg aggaagctgg gatacagcat ttaatgaaaa atttatgctt      60
aagaagtaaa a atg gca ggc ttc cta gat aat ttt cgt tgg cca gaa tgt      110
      Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys
      -40                                -35
gaa tgt att gac tgg agt gag aga aga aat gct gtg gca tct gtt gtc      158
Glu Cys Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val
      -30                                -25                                -20
gca ggt ata ttg ttt ttt aca ggc tgg tgg ata atg att gat gca gct      206
Ala Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
      -15                                -10                                -5                                1
gtg gtg tat cct aag cca gaa cag ttg aac cat gcc ttt cac aca tgt      254
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys
      5                                10                                15
ggg gta ttt tcc aca ttg gct ttc ttc atg ata aat gct gta tcc aat      302
Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn
      20                                25                                30
gct cag gtg aga ggt gat agc tat gaa agc ggc tgt tta gga aga aca      350
Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr
      35                                40                                45
ggg gct cga gtt tgg ctt ttc att ggt ttc atg ttg atg ttt ggg tca      398
Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser
      50                                55                                60                                65
ctt att gct tcc atg tgg att ctt ttt ggt gca tat gtt acc caa aat      446
Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn
      70                                75                                80
act gat gtt tat ccg gga cta gct gtg ttt ttt caa aat gca ctt ata      494
Thr Asp Val Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile
      85                                90                                95
ttt ttt agc act ctg atc tac aaa ttt gga aga acc gaa gag cta tgg      542
Phe Phe Ser Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp
      100                                105                                110
acc tgagatcact tcttaagtca ctttttccct ttgttatatt ctgtttgtag      595
Thr
atagggttttt tatctctcag tacacattgc caaatggagt agattgtaca ttaaattgttt      655
tggtttcttta catttttatg ttctgagttt tgaaatagtt ttatgaaatt tctttatgtt      715
tcattgcata gactgttaat atgtatataa tacaagacta tatgaattgg ataattgagta      775
tcagtttttt attcctgaga tttagaactt gatctactcc ctgagccagg gttacatcat      835
cttgtcattt tagaagtaac cactcttgct tctctggctg ggcacggtgg ctcatgcctg      895
taatcccagc actttgggag gccgaggcgg gccgattgct tgaggtcaag tgtttgagac      955
cagcctggcc aacatggcga aaccccatct actaaaaata caaaaattag ccaggcatgg      1015
tggtgggtgc ctgtaatccc aactacctag gaggtgagg caggagaatc gcttgaacct      1075
ggggggcaga gggtgyagt agctgagttt gcgccactgc actctagcct gggggagaaa      1135
gtgaaactcc ctctcaaaaa aaaaaaamc      1164

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<210> 375

<211> 1250

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 36..425

<220>

<221> sig_peptide

<222> 36..119

<223> Von Heijne matrix

score 11.6000003814697
seq LLLLVQLLRFLRA/DG

<220>

<221> polyA_signal

<222> 1215..1220

<220>

<221> polyA_site

<222> 1240..1250

<220>

<221> misc_feature

<222> 576

<223> n=a, g, c or t

<400> 375

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atttcttccc cccgagctgg gcgtgcgcgg ccgca atg aac tgg gag ctg ctg      53
                                Met Asn Trp Glu Leu Leu
                                -25
ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc ttg gtg cag ctg      101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Val Gln Leu
      -20                                -15                                -10
ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta cta tgg gcc gag      149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
      -5                                1                                5                                10
tgg cag gga cga cgc cca gaa tgg gag ctg act gat atg gtg gtg tgg      197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
                                15                                20                                25
gtg act gga gcc tcg agt gga att ggt gag gag ctg gct tac cag ttg      245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
                                30                                35                                40
tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga aga gtg cat gag      293
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg Arg Val His Glu
                                45                                50                                55
ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc aat tta aaa gaa      341
Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly Asn Leu Lys Glu
                                60                                65                                70
aaa gat ata ctt gtt ttg ccc ctt gac ctg acc act ggt tcc cat      389
Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp Thr Gly Ser His
                                75                                80                                85                                90
gaa agc ggc tac caa agc tgt tct cca gga att tgg tagaatcgac      435
Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly Ile Trp
                                95                                100
attctgggtca acaatgtgga aatgtcccag cgttctctgt gcatggatac caacttggat      495
gtctacagaa agctaattgag agcttaacta cttagggacg gtgtccttga caaatgtgk      555
kctgcctcac atgatcgaga ngaarcaagg aaagattggt actgtgaata gcatcctggg      615
tatcatatct gtacctcttt ccattggata ctgtgctagc aagcatgctc tccggggktk      675
ktttaatggc cttcraacag aacttgccac ataccargt ataatagttt ctaacatttg      735
cccaggacct gtgcaatcaa atattgtgga aaattcccta gctggagaag tcacaaagac      795
tataggcaat aatggagacc agtcccacaa gatgacaacc agtcgtttgtg tgcggctgat      855
gttaatcagc atggccaatg atttgaaaga agtttggatc tcagaacaac ctttcttggt      915
agtaacatat ttgtggcaat acatgccaac ctgggccttg tggataacca acaagatggg      975
gaagaaaagg attgagaact ttaagagtgg tgtggatgca gactcttctt attttaaaat      1035
ctttaagaca aaacatgact gaaaagagca cctgtacttt tcaagccact ggagggagaa      1095
atggaaaaca tgaaaacagc aatcttctta tgcttctgaa taatcaaaga ctaatttggt      1155
attttacttt ttaatagata tgactttgct tccaacatgg aatgaaataa aaaataaata      1215

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ataaaagatt gccatgaatc ttgcaaaaaa aaaaa

1250

<210> 376

<211> 947

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 155..751

<220>

<221> sig_peptide

<222> 155..340

<223> Von Heijne matrix
score 3.70000004768372
seq SILGIISVPLSIG/YC

<220>

<221> polyA_signal

<222> 912..917

<220>

<221> polyA_site

<222> 937..947

<220>

<221> misc_feature

<222> 760

<223> n=a, g, c or t

<400> 376

agtgaaaaga agatgcctag agaatggcaa tttaaaagaa aaagatatatc ttgttttgcc	60
ccttgacctg accgacactg gttcccatga agcggctacc aaagctgttc tccaggagtt	120
tggtagaatc gacattctgg tcaacaatgg tgga atg tcc cag cgt tct ctg tgc	175
Met Ser Gln Arg Ser Leu Cys	
-60	
atg gat acc agc ttg gat gtc tac aga rag cta ata gag ctt aac tac	223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr	
-55 -50 -45 -40	
tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc gag	271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu	
-35 -30 -25	
agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc ata	319
Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile	
-20 -15 -10	
tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc cgg	367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg	
-5 1 5	
ggg ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt ata	415
Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile	
10 15 20 25	
ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg gaa	463
Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu	
30 35 40	
aat tcc cta gct gga gaa gtc aca aaa act ata ggc aat aat gga aac	511
Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asn	

	45		50		55	
cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta atc						559
Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile						
	60		65		70	
agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct ttc						607
Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro Phe						
	75		80		85	
ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg tgg						655
Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp Trp						
	90		95		100	105
ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt ggt						703
Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser Gly						
	110		115		120	
gtg gat gcm rac tct tct tat ttt aaa atc ttt aag aca aaa cat gac						751
Val Asp Ala Xaa Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His Asp						
	125		130		135	
tgaaaaganc acctgtactt ttcaagccac tggagggaga aatggaaaac atgaaaacag						811
caatcttctt atgcttctga ataatacaag actaatttgt gattttactt tttaatagat						871
atgactttgc ttccaacatg grrtgaaata aaaaataaat aataaaaagat tgccatgrrt						931
cttgcaaaaa aaaaaa						947

<210> 377
 <211> 621
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..585

<220>
 <221> sig_peptide
 <222> 46..120
 <223> Von Heijne matrix
 score 6.30000019073486
 seq AFSLSVMAALTFG/CF

<220>
 <221> polyA_signal
 <222> 584..589

<220>
 <221> polyA_site
 <222> 606..619

<400> 377	
aactgggtgt gcgtrtggag tccggactcg tgggagacga tcgcg atg aac acg gtg	57
	Met Asn Thr Val
	-25
ctg tcg cgg gcg aac tca ctg ttc gcc ttc tcg ctg agc gtg atg gcs	105
Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu Ser Val Met Ala	
	-20 -15 -10
gcg ctc acc ttc ggc tgc ttc atc ayy acc gcc ttc aaa gac agg agc	153
Ala Leu Thr Phe Gly Cys Phe Ile Xaa Thr Ala Phe Lys Asp Arg Ser	
	-5 1 5 10
gtc ccg gtg cgg ctg cac gtc tcg cga atc atg cta aaa aat gta gaa	201
Val Pro Val Arg Leu His Val Ser Arg Ile Met Leu Lys Asn Val Glu	

	15		20		25	
gat ttc act gga cct aga gaa aga agt gat ctg gga ttt atc aca ttt						249
Asp Phe Thr Gly Pro Arg Glu Arg Ser Asp Leu Gly Phe Ile Thr Phe						
	30		35		40	
gat ata act gct gat cta gag aat ata ttt gat tgg aat gtt aag cag						297
Asp Ile Thr Ala Asp Leu Glu Asn Ile Phe Asp Trp Asn Val Lys Gln						
	45		50		55	
ttg ttt ctt tat tta tca gca gaa tat tca aca aaa aat aat gct ctg						345
Leu Phe Leu Tyr Leu Ser Ala Glu Tyr Ser Thr Lys Asn Asn Ala Leu						
	60		65		70	75
aac caa ktt gtc cta tgg gac aag att gtt ttg aga ggt gat aat ccg						393
Asn Gln Xaa Val Leu Trp Asp Lys Ile Val Leu Arg Gly Asp Asn Pro						
	80		85		90	
aag ctg ctg ctg aaa gat atg aaa aca aaa tat ttt ttc ttt gac gat						441
Lys Leu Leu Leu Lys Asp Met Lys Thr Lys Tyr Phe Phe Phe Asp Asp						
	95		100		105	
gga aat ggt ctc wag gga aac agg aat gtc act ttg acc ctg tct tgg						489
Gly Asn Gly Leu Xaa Gly Asn Arg Asn Val Thr Leu Thr Leu Ser Trp						
	110		115		120	
aac gtc gta cca aat gct gga att cta cct ctt gtg aca gga tca gga						537
Asn Val Val Pro Asn Ala Gly Ile Leu Pro Leu Val Thr Gly Ser Gly						
	125		130		135	
cac gta tct gtc cca ttt cca gat aca tat gaa ata acg aag agt tat						585
His Val Ser Val Pro Phe Pro Asp Thr Tyr Glu Ile Thr Lys Ser Tyr						
	140		145		150	155
taaattatttc tgaatttgaa acaaaaaaaaaaaa aaaahm						621

<210> 378
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<220>
 <221> UNSURE
 <222> 12
 <223> Xaa = any one of the twenty amino acids

<400> 378	
Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val Leu Gln Leu Thr Thr	
-20	-15 -10 -5
Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val Asn Pro Phe Glu Xaa	
	1 5 10
Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala His His Phe Ile His	
	15 20 25
Pro Cys Leu Asp	
30	

<210> 379
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -23..-1

<220>
 <221> UNSURE
 <222> -8
 <223> Xaa = any one of the twenty amino acids

<400> 379
 Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu Pro Pro Leu Xaa
 -20 -15 -10
 Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro Glu Arg Gly Ala
 -5 1 5
 Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg Phe Cys Pro Pro
 10 15 20 25
 Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp Lys Tyr Ser Asn
 30 35 40
 Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu Ser Pro Leu Glu
 45 50 55
 Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu Trp Asn Gln Gln
 60 65 70
 Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu Lys Glu Glu Phe
 75 80 85
 Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu Arg Thr Glu Ser
 90 95 100 105
 Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala Asp Phe Tyr Lys
 110 115 120
 Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr Tyr Asn Arg Asp
 125 130 135
 Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly Lys Val Ala
 140 145 150
 Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys Lys Arg Ser
 155 160 165
 Asn
 170

<210> 380
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1
 <220>
 <221> UNSURE
 <222> -9,37,38,40
 <223> Xaa = any one of the twenty amino acids

<400> 380
 Met Ala Phe Thr Leu Xaa Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
 -10 -5 1
 Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
 5 10 15
 Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
 20 25 30

Lys Ser Xaa Xaa Met Xaa Leu Ile Arg Ser Val Arg Thr Val Met Arg
 35 40 45 50
 Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
 55 60 65
 Phe Gly

<210> 381
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<220>
 <221> UNSURE
 <222> 85,89,113,114,117,118,136,150,153,161,162,164
 <223> Xaa = any one of the twenty amino acids

<400> 381
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
 -20 -15 -10
 Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
 -5 1 5 10
 Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
 15 20 25
 Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu Thr Lys Ala Arg
 30 35 40
 Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
 45 50 55
 Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
 60 65 70 75
 Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu Gln Ala Xaa Ala Thr
 80 85 90
 Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
 95 100 105
 Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa Ala Trp Leu Gly Pro
 110 115 120
 Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro Pro Xaa Lys Gln Asn
 125 130 135
 His Ile Leu Trp Ala Leu Thr Gly His Val Xaa Arg Gln Xaa Arg Glu
 140 145 150 155
 Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile Gln Glu Lys Leu His
 160 165 170
 Thr Ala Ala Leu Pro Ala
 175

<210> 382
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<220>
 <221> UNSURE
 <222> 98
 <223> Xaa = any one of the twenty amino acids

<400> 382

Met	Asp	Lys	Leu	Lys	Lys	Val	Leu	Ser	Gly	Gln	Asp	Thr	Glu	Asp	Arg
-55				-50					-45						-40
Ser	Gly	Leu	Ser	Glu	Val	Val	Glu	Ala	Ser	Ser	Leu	Ser	Trp	Ser	Thr
			-35					-30						-25	
Arg	Ile	Lys	Gly	Phe	Ile	Ala	Cys	Phe	Ala	Ile	Gly	Ile	Leu	Cys	Ser
		-20					-15						-10		
Leu	Leu	Gly	Thr	Val	Leu	Leu	Trp	Val	Pro	Arg	Lys	Gly	Leu	His	Leu
	-5					1			5						
Phe	Ala	Val	Phe	Tyr	Thr	Phe	Gly	Asn	Ile	Ala	Ser	Ile	Gly	Ser	Thr
10				15				20						25	
Ile	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Arg	Met	Phe	Glu	Pro
			30					35					40		
Thr	Arg	Leu	Ile	Ala	Thr	Ile	Met	Val	Leu	Leu	Cys	Phe	Ala	Leu	Thr
		45					50					55			
Leu	Cys	Ser	Ala	Phe	Trp	Trp	His	Asn	Lys	Gly	Leu	Ala	Leu	Ile	Phe
	60					65					70				
Cys	Ile	Leu	Gln	Ser	Leu	Ala	Leu	Thr	Trp	Tyr	Ser	Leu	Ser	Phe	Ile
	75				80					85					
Pro	Phe	Ala	Arg	Asp	Ala	Val	Lys	Xaa	Cys	Phe	Ala	Val	Cys	Leu	Ala
90					95					100					105

<210> 383
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 383

Met	Lys	Ala	Leu	Cys	Leu	Leu	Leu	Leu	Pro	Val	Leu	Gly	Leu	Leu	Val
		-15						-10				-5			
Ser	Ser	Lys	Thr	Leu	Cys	Ser	Met	Glu	Glu	Ala	Ile	Asn	Glu	Arg	Ile
	1				5						10				
Gln	Glu	Val	Ala	Gly	Ser	Leu	Ile	Phe	Arg	Ala	Ile	Ser	Ser	Ile	Gly
15				20					25					30	
Arg	Gly	Ser	Glu	Ser	Val	Thr	Ser	Arg	Gly	Asp	Leu	Ala	Thr	Cys	Pro
			35					40					45		
Arg	Gly	Phe	Ala	Val	Thr	Gly	Cys	Thr	Cys	Gly	Ser	Ala	Cys	Gly	Ser
		50					55					60			
Trp	Asp	Val	Arg	Ala	Glu	Thr	Thr	Cys	His	Cys	Gln	Cys	Ala	Gly	Met
	65					70					75				
Asp	Trp	Thr	Gly	Ala	Arg	Cys	Cys	Arg	Val	Gln	Pro				
	80					85					90				

<210> 384
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<220>
 <221> UNSURE
 <222> 15,17,40
 <223> Xaa = any one of the twenty amino acids

<400> 384
 Met Ile Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu
 -20 -15 -10
 Phe Pro Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp
 -5 1 5 10
 Leu Tyr Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser
 15 20 25
 Gln Lys Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
 30 35 40

<210> 385
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<220>
 <221> UNSURE
 <222> -11
 <223> Xaa = any one of the twenty amino acids

<400> 385
 Met Gly Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser
 -15 -10 -5 1
 Ala Lys Pro Asn Glu Gln Pro Trp Leu Leu Asn
 5 10

<210> 386
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<220>
 <221> UNSURE
 <222> 72,74,95,98,101,102,105,125
 <223> Xaa = any one of the twenty amino acids

<400> 386
 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
 -20 -15 -10
 Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser

-5					1				5					10
Ala	Asp	Ser	Thr	Ile	Met	Asp	Ile	Gln	Val	Pro	Thr	Arg	Ala	Pro
			15					20					25	
Ala	Val	Tyr	Thr	Glu	Leu	Gln	Pro	Thr	Ser	Pro	Thr	Pro	Thr	Trp
		30					35					40		
Ala	Asp	Glu	Thr	Pro	Gln	Pro	Gln	Thr	Gln	Thr	Gln	Gln	Leu	Glu
	45					50				55				
Thr	Asp	Gly	Pro	Leu	Val	Thr	Asp	Pro	Glu	Thr	His	Xaa	Ser	Xaa
60					65					70				75
Ala	Ala	His	Pro	Thr	Asp	Asp	Thr	Thr	Thr	Leu	Ser	Glu	Arg	Pro
			80					85					90	
Pro	Ser	Thr	Xaa	Val	His	Xaa	Arg	Pro	Xaa	Xaa	Pro	Ser	Xaa	His
		95					100						105	
Val	Phe	Met	Arg	Met	Thr	Pro	Ser	Ser	Met	Met	Asn	Thr	Pro	Ser
	110						115				120			
Asn	Xaa	Gly	Cys	Trp	Ser	Gln	Leu	Cys	Cys	Ser	Ser	Gln	Ala	Ser
	125					130				135				
Ser	Ser	Pro	Val	Ala	Ser	Ala	Gly	Ser	Cys	Pro	Gly	Tyr	Ala	Gly
140					145					150				155
Ile	Ala	Gly	Glu	Ser	Ile	Arg	Asn	Arg	Ser					
				160				165						

<210> 387

<211> 179

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<220>

<221> UNSURE

<222> 36,63,103,128,131,139,140,152

<223> Xaa = any one of the twenty amino acids

<400> 387

Met	Glu	Thr	Gly	Ala	Leu	Arg	Arg	Pro	Gln	Leu	Leu	Pro	Leu	Leu
	-25					-20					-15			
Leu	Leu	Cys	Gly	Pro	Ser	Gln	Asp	Gln	Cys	Arg	Pro	Val	Leu	Gln
-10					-5				1				5	Asn
Leu	Leu	Gln	Ser	Pro	Gly	Leu	Thr	Trp	Ser	Leu	Glu	Val	Pro	Thr
		10					15					20		Gly
Arg	Glu	Gly	Lys	Glu	Gly	Gly	Asp	Arg	Gly	Pro	Gly	Leu	Xaa	Gly
	25					30					35			Ala
Thr	Pro	Ala	Arg	Ser	Pro	Gln	Gly	Lys	Glu	Met	Gly	Arg	Gln	Arg
	40					45				50				Thr
Arg	Lys	Val	Lys	Gly	Pro	Ala	Trp	Xaa	His	Thr	Ala	Asn	Gln	Glu
55					60					65				70
Asn	Arg	Met	Arg	Ser	Leu	Ser	Ser	Gly	Ser	Val	Pro	Val	Gly	His
			75					80					85	Leu
Glu	Gly	Gly	Thr	Val	Lys	Leu	Gln	Lys	Asp	Thr	Gly	Leu	His	Ser
		90					95					100		Cys
Xaa	Asp	Gly	Met	Ala	Ser	Leu	Glu	Gly	Thr	Pro	Ala	Ser	Val	Leu
	105					110					115			Ala
Asp	Ala	Cys	Pro	Gly	Phe	His	Asp	Val	Xaa	Val	Gln	Xaa	Ala	Leu
	120					125					130			Phe

Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys Thr His Phe Cys Leu Ser
 135 140 145 150
 Ile Xaa Leu

<210> 388
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55..-1

<400> 388
 Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys
 -55 -50 -45 -40
 Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu
 -35 -30 -25
 Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr
 -20 -15 -10
 Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met
 -5 1 5
 Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly
 10 15 20 25
 Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr
 30 35 40
 Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu
 45 50 55
 Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala
 60 65 70
 Pro Phe Pro Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser
 75 80 85
 Pro Gly Cys Tyr Arg Tyr
 90 95

<210> 389
 <211> 236
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<220>
 <221> UNSURE
 <222> 28,30,40,67,86,117,120
 <223> Xaa = any one of the twenty amino acids

<400> 389
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Lys
 -30 -25 -20
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala
 -15 -10 -5 1
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 5 10 15
 Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro Asp Leu

Gly Tyr Leu Met Gly
45

<210> 391
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<220>
<221> UNSURE
<222> -1,1
<223> Xaa = any one of the twenty amino acids

<400> 391
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
 -45 -40 -35
Leu Thr Pro Cys Leu Thr Val Pro Arg Pro Leu Phe Leu Leu Leu
 -30 -25 -20
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
 -15 -10 -5
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
 1 5 10 15
Phe Phe Ile Pro Asp
 20

<210> 392
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<220>
<221> UNSURE
<222> 58
<223> Xaa = any one of the twenty amino acids

<400> 392
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-30 -25 -20 -15
Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
 -10 -5 1
Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
 5 10 15
Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
 20 25 30
Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
35 40 45 50
Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg Glu Ala Leu
 55 60 65
Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp

Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa
 25 30 35
 Ser

<210> 395
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<220>
 <221> UNSURE
 <222> 35,37,39,40
 <223> Xaa = any one of the twenty amino acids

<400> 395
 Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe Leu Ser Tyr Leu Pro
 -20 -15 -10
 Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly Ser Thr Leu Gly Lys
 -5 1 5
 Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg Pro Trp Asp Ala Ala
 10 15 20
 Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa Asn Xaa Tyr Xaa Xaa
 25 30 35 40
 Trp Gly Gln Gly Thr His Ser Ser Leu
 45

<210> 396
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 396
 Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro Thr
 -15 -10 -5
 Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg Leu
 1 5 10
 Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala Leu
 15 20 25 30
 Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
 35 40

<210> 397
 <211> 192
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -93..-1

<220>
 <221> UNSURE
 <222> 21,28,39,42
 <223> Xaa = any one of the twenty amino acids

<400> 397
 Met Ala Glu Leu Gly Leu Asn Glu His His Gln Asn Glu Val Ile Asn
 -90 -85 -80
 Tyr Met Arg Phe Ala Arg Ser Lys Arg Gly Leu Arg Leu Lys Thr Val
 -75 -70 -65
 Asp Ser Cys Phe Gln Asp Leu Lys Glu Ser Arg Leu Val Glu Asp Thr
 -60 -55 -50
 Phe Thr Ile Asp Glu Val Ser Glu Val Leu Asn Gly Leu Gln Ala Val
 -45 -40 -35 -30
 Val His Ser Glu Val Glu Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn
 -25 -20 -15
 Val Leu Leu Leu Arg Gln Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu
 -10 -5 1
 Lys Leu Gln Thr Asp Ile Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu
 5 10 15
 Gln Xaa Ala Glu Phe Glu Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys
 20 25 30 35
 Pro Ile Leu Xaa Val Thr Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly
 40 45 50
 Gly Thr Ala Lys Leu Leu Asn Lys Val Ile Cys Ile Ile Leu Arg Asn
 55 60 65
 Gly Lys Ser Leu Ile Leu Ser Cys His Cys Leu Gly Trp Arg Asn Lys
 70 75 80
 Ser Gly Arg Phe Val Ser Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
 85 90 95

<210> 398
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -72...-1

<400> 398
 Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
 -70 -65 -60
 Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
 -55 -50 -45
 Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
 -40 -35 -30 -25
 Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala
 -20 -15 -10
 Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala
 -5 1 5
 Ser Asp Trp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Ser Val
 10 15 20
 Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala Pro Gly Pro Tyr
 25 30 35 40
 Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro Val Ala Pro Gln

				45					50					55			
His	Thr	Leu	Lys	Leu	Ile	Thr	Tyr	Val	Lys	Lys	Asn	Gln	Lys	Thr	Leu		
			60					65					70				
Phe	Ser	Met	Val	Gly													
			75														

<210> 399
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<220>
 <221> UNSURE
 <222> 51
 <223> Xaa = any one of the twenty amino acids

<400> 399																	
Met	Thr	Pro	Leu	Leu	Thr	Leu	Ile	Leu	Val	Val	Leu	Met	Gly	Leu	Pro		
-20					-15					-10					-5		
Leu	Ala	Gln	Ala	Leu	Asp	Cys	His	Val	Cys	Ala	Tyr	Asn	Gly	Asp	Asn		
				1				5					10				
Cys	Phe	Asn	Pro	Met	Arg	Cys	Pro	Ala	Met	Val	Ala	Tyr	Cys	Met	Thr		
		15					20					25					
Thr	Arg	Thr	Tyr	Tyr	Thr	Pro	Thr	Arg	Met	Lys	Val	Ser	Lys	Ser	Cys		
	30					35					40						
Val	Pro	Arg	Cys	Phe	Glu	Xaa	Cys	Val									
45						50											

<210> 400
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<220>
 <221> UNSURE
 <222> 62
 <223> Xaa = any one of the twenty amino acids

<400> 400																	
Met	Asn	Leu	His	Phe	Pro	Gln	Trp	Phe	Val	His	Ser	Ser	Ala	Leu	Gly		
-20					-15					-10					-5		
Leu	Val	Leu	Ala	Pro	Pro	Phe	Ser	Ser	Pro	Gly	Thr	Asp	Pro	Thr	Phe		
				1				5					10				
Pro	Cys	Ile	Tyr	Cys	Arg	Leu	Leu	Asn	Met	Ile	Met	Thr	Arg	Leu	Ala		
		15				20					25						
Phe	Ser	Phe	Ile	Thr	Cys	Leu	Cys	Pro	Asn	Leu	Lys	Glu	Val	Cys	Leu		
	30					35					40						
Ile	Leu	Pro	Glu	Lys	Asn	Cys	Asn	Ser	Arg	His	Ala	Gly	Phe	Val	Gly		
45					50					55					60		

Pro Xaa Lys Leu Arg Gln
65

<210> 401
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<220>
<221> UNSURE
<222> 12
<223> Xaa = any one of the twenty amino acids

<400> 401
Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala Cys Gly Ser Leu Leu
-20 -15 -10
Pro Gly Leu Trp Gln His Leu Thr Ala Asn His Trp Pro Pro Phe Ser
-5 1 5 10
Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser Glu Gln Ile Ser Glu
15 20 25
Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg Ser Leu Asn Gln Glu
30 35 40
Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr Ser Ile Thr
45 50 55

<210> 402
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 402
Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu Pro Leu Ser
-25 -20 -15
Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser
-10 -5 1
Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val Pro Glu Pro
5 10 15 20
Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg
25 30 35
Thr

<210> 403
<211> 211
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<220>
 <221> UNSURE
 <222> 10,87,93,96,106,109,111,118,122,159,171,176
 <223> Xaa = any one of the twenty amino acids

<400> 403
 Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu Glu Leu Thr
 -25 -20 -15
 Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr Asn Lys Phe
 -10 -5 1 5
 Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile Phe Ile Gly
 10 15 20
 Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu Ser Lys Asn
 25 30 35
 Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile Leu Val His
 40 45 50
 Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly Asp Ala Pro
 55 60 65
 Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile Lys Ser Ser
 70 75 80 85
 Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu Gly Asn Ser
 90 95 100
 Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu Tyr Ser Glu
 105 110 115
 Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln Ser Ile Cys
 120 125 130
 Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu His Trp Gln
 135 140 145
 Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile Ser Phe Phe
 150 155 160 165
 Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly Ser Asp Tyr
 170 175 180
 Arg Ser Ile

<210> 404
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -80..-1

<220>
 <221> UNSURE
 <222> 36
 <223> Xaa = any one of the twenty amino acids

<400> 404
 Met Ser Thr Trp Tyr Leu Ala Leu Asn Lys Ser Tyr Lys Asn Lys Asp
 -80 -75 -70 -65
 Ser Val Arg Ile Tyr Leu Ser Leu Cys Thr Val Ser Ile Lys Phe Thr
 -60 -55 -50
 Tyr Phe His Asp Ile Gln Thr Asn Cys Leu Thr Thr Trp Lys His Ser
 -45 -40 -35
 Arg Cys Arg Phe Tyr Trp Ala Phe Gly Gly Ser Ile Leu Gln His Ser

Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
 5 10 15
 Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
 20 25 30
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
 35 40 45
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn
 50 55 60 65
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
 70 75 80
 Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser His Val Ser
 85 90 95
 Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys
 100 105 110
 Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp Asn Trp Glu
 115 120 125
 Pro Asn
 130

<210> 407
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<220>
 <221> UNSURE
 <222> 26,28,50
 <223> Xaa = any one of the twenty amino acids

<400> 407
 Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
 -35 -30 -25
 Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
 -20 -15 -10
 Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
 -5 1 5 10
 Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Xaa Gln
 15 20 25
 Xaa Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
 30 35 40
 Gly Phe Ser Phe Cys Gln Xaa Arg Leu Asn Lys Arg Lys Glu Tyr Met
 45 50 55
 Val Arg
 60

<210> 408
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<220>
 <221> UNSURE
 <222> 9,10,12,16
 <223> Xaa = any one of the twenty amino acids

 <400> 408
 Met Arg Phe Leu Pro Cys Cys Leu Leu Trp Ser Val Phe Asn Pro Glu
 -15 -10 -5 1
 Ser Leu Asn Cys His Tyr Phe Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser
 5 10 15
 Leu Gln Tyr Tyr Glu Ile Ser Leu Gln Glu Lys Leu Leu Gly Phe Leu
 20 25 30
 Trp Leu Cys Phe Leu Ser Tyr Phe Phe Arg Ala Val Tyr Phe Leu Ile
 35 40 45
 Asp Phe Ser Ser Phe Thr
 50 55

<210> 409
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45..-1

<400> 409
 Met His Ser Leu Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser
 -45 -40 -35 -30
 Phe Ser Phe Arg Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly
 -25 -20 -15
 Glu Asn Phe Leu Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser
 -10 -5 1
 Gly Ser Thr Phe Met Arg Asp Ile Glu Thr Asn Lys
 5 10 15

<210> 410
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<220>
 <221> UNSURE
 <222> 8,9
 <223> Xaa = any one of the twenty amino acids

<400> 410
 Met Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser
 -20 -15 -10
 Ser Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys
 -5 1 5 10
 Asn Pro Phe Leu Trp Lys Leu

<210> 411
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<220>
 <221> UNSURE
 <222> 13,24
 <223> Xaa = any one of the twenty amino acids

<400> 411
 Met Ala Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala
 -20 -15 -10
 Phe Pro Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly
 -5 1 5
 Lys Pro Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg
 10 15 20 25
 Ile Trp Pro

<210> 412
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48..-1

<220>
 <221> UNSURE
 <222> 12,13,33,34
 <223> Xaa = any one of the twenty amino acids

<400> 412
 Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
 -45 -40 -35
 Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
 -30 -25 -20
 Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
 -15 -10 -5
 Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Xaa Xaa Cys Cys Cys
 1 5 10 15
 Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
 20 25 30
 Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
 35 40 45

<210> 413
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -32...-1

<400> 413

```
Met Asp Glu Tyr Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly
      -30                      -25                      -20
Gln Met Phe Thr Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys
      -15                      -10                      -5
Gln Arg Phe Phe Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser
1          5          10          15
Thr Val Thr Pro Ser Trp Arg Leu Cys Leu Val Ser
      20          25
```

<210> 414

<211> 170

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -79...-1

<220>

<221> UNSURE

<222> 7,8,17,49,52,54,68,77

<223> Xaa = any one of the twenty amino acids

<400> 414

```
Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
      -75                      -70                      -65
Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
      -60                      -55                      -50
Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe
      -45                      -40                      -35
Gln Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
      -30                      -25                      -20
Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
      -15                      -10                      -5          1
Pro Ser Ser Lys Ala Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa
      5          10          15
Ala Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe
      20          25          30
Pro Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa
      35          40          45
Arg His Xaa Gln Xaa His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala
50          55          60          65
Cys Thr Xaa Cys Gly Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln
      70          75          80
His Tyr Ile Arg His Ala Arg Gly Gly Leu
      85          90
```

<210> 415

<211> 190

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -82...-1

<220>
 <221> UNSURE
 <222> 26,54,84
 <223> Xaa = any one of the twenty amino acids

<400> 415
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
 -15 -10 -5
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
 1 5 10
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp Ile
 15 20 25 30
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
 35 40 45
 Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala Leu
 50 55 60
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
 65 70 75
 Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg His
 80 85 90
 Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
 95 100 105

<210> 416
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 416
 Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
 -60 -55 -50 -45
 Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
 -40 -35 -30
 Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
 -25 -20 -15
 Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
 -10 -5 1
 Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
 5 10 15 20
 Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Lys

25 30 35
 Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser
 40 45 50
 Ser Lys

<210> 417
 <211> 161
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -108...-1

<220>
 <221> UNSURE
 <222> -99
 <223> Xaa = any one of the twenty amino acids

<400> 417
 Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln Ser Pro Gln Ala Leu
 -105 -100 -95
 Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser Ile Thr Leu Thr Leu
 -90 -85 -80
 Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg Asn Val Thr His Leu
 -75 -70 -65
 Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu Ser Gly Arg Glu Ala
 -60 -55 -50 -45
 His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro Thr Ala Trp Ser Ser
 -40 -35 -30
 Asp Asp Cys Ala Leu His Gly His Cys Glu Gln Val Val Phe Thr Ala
 -25 -20 -15
 Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe Pro Ser Leu Tyr Ser
 -10 -5 1
 His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr Pro Arg Ser Gly Thr
 5 10 15 20
 Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln Asn Thr Pro Lys Ile
 25 30 35
 Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu Glu Lys Ser Ile Met
 40 45 50
 Leu

<210> 418
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 418
 Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
 -20 -15 -10
 Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
 -5 1 5 10
 Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val

15 20 25
 Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
 30 35 40
 Leu Arg Met
 45

<210> 419
 <211> 332
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<220>
 <221> UNSURE
 <222> -30,108,134,139,140,154,206,217
 <223> Xaa = any one of the twenty amino acids

<400> 419
 Met Ile Xaa Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp
 -30 -25 -20
 Thr Arg Gln Leu Pro Leu Leu Thr Ser Ala Leu His Gly Leu Gln Gln
 -15 -10 -5
 Gln His Pro Ala Phe Ser Gly Val Ala Arg Leu Ala Lys Arg Trp Val
 1 5 10 15
 Arg Ala Gln Leu Leu Gly Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu
 20 25 30
 Val Ala Ala Ala Leu Phe Leu His Pro Glu Pro Phe Thr Pro Pro Ser
 35 40 45
 Ser Pro Gln Val Gly Phe Leu Arg Phe Leu Phe Leu Val Ser Thr Phe
 50 55 60
 Asp Trp Lys Asn Asn Pro Leu Phe Val Asn Leu Asn Asn Glu Leu Thr
 65 70 75 80
 Val Glu Glu Gln Val Glu Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala
 85 90 95
 Gln Leu Pro Val Met Val Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser
 100 105 110
 Val Trp Thr Gln Asp Gly Pro Ser Ala Gln Ile Leu Gln Gln Leu Val
 115 120 125
 Val Leu Ala Ala Glu Xaa Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp
 130 135 140
 Pro Arg Gly Pro Gly Asp Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp
 145 150 155 160
 Ile Tyr Asp Val Leu Ile Arg Leu Ser Pro Arg His Ile Pro Arg His
 165 170 175
 Arg Gln Ala Val Asp Ser Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu
 180 185 190
 Ser Gln Pro Gly Pro Ser Ser Leu Met Pro Val Leu Gly Xaa Asp Pro
 195 200 205
 Pro Gln Leu Tyr Leu Thr Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala
 210 215 220
 Leu Phe Phe Tyr Asp Gln His Gly Gly Glu Val Ile Gly Val Leu Trp
 225 230 235 240
 Lys Pro Thr Ser Phe Gln Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys
 245 250 255

Gly Arg Met Val Met Ser Arg Gly Gly Glu Leu Val Met Val Pro Asn
260 265 270
Val Glu Ala Ile Leu Glu Asp Phe Ala Val Leu Gly Glu Gly Leu Val
275 280 285
Gln Thr Val Glu Ala Arg Ser Glu Arg Trp Thr Val
290 295 300

<210> 420
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19...-1

<400> 420
Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser Phe His
-15 -10 -5
Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser Arg His
1 5 10
His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu Glu Asn
15 20 25
Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys Ile Val
30 35 40 45
Gly

<210> 421
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30...-1

<220>
<221> UNSURE
<222> 23
<223> Xaa = any one of the twenty amino acids

<400> 421
Met Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser
-30 -25 -20 -15
Thr Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val
-10 -5 1
Arg Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala
5 10 15
Glu Glu Gln Lys Xaa Ser Gly Ile Met
20 25

<210> 422
<211> 85
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -17..-1

<220>
<221> UNSURE
<222> 24
<223> Xaa = any one of the twenty amino acids

<400> 422
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
-15 -10 -5
Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser
1 5 10 15
Asp Ser Asp Glu Leu Ala Ser Gly Xaa Phe Val Phe Pro Tyr Pro Tyr
20 25 30
Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
35 40 45
Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
50 55 60
Leu Pro Ser Glu Lys
65

<210> 423
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<220>
<221> UNSURE
<222> 7
<223> Xaa = any one of the twenty amino acids

<400> 423
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
-15 -10 -5
Gly Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser
1 5 10 15
Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
20 25 30
Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
35 40 45
Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
50 55 60
Leu Pro Ser Glu Lys
65

<210> 424
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -29..-1

<220>

<221> UNSURE

<222> 24,26,34,37

<223> Xaa = any one of the twenty amino acids

<400> 424

Met	Thr	Cys	Arg	Gly	Ser	Cys	Ser	Tyr	Ala	Thr	Arg	Arg	Ser	Pro	Ser	
				-25					-20					-15		
Glu	Leu	Ser	Leu	Leu	Pro	Ser	Ser	Leu	Trp	Val	Leu	Ala	Thr	Ser	Ser	
			-10					-5					1			
Pro	Thr	Ile	Thr	Ile	Ala	Leu	Ala	Met	Ala	Ala	Gly	Asn	Leu	Cys	Pro	
	5					10				15						
Leu	Pro	Ser	Ser	Xaa	Arg	Xaa	Lys	Arg	Arg	Trp	Cys	Gln	Ala	Xaa	Gln	
20					25					30					35	
Gln	Xaa	Ala	Leu	Leu												
				40												

<210> 425

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -56..-1

<220>

<221> UNSURE

<222> -13,4

<223> Xaa = any one of the twenty amino acids

<400> 425

Met	Val	Pro	Trp	Pro	Arg	Gly	Lys	Val	Lys	Thr	Ala	Pro	Ile	Pro	Ile	
	-55					-50					-45					
Ser	Arg	Phe	Pro	Phe	Leu	Pro	Thr	His	Asp	Pro	Pro	Thr	Pro	Ala	His	
-40					-35				-30						-25	
Trp	Ser	Pro	Ala	Ser	His	Gln	Gln	Phe	Lys	His	Xaa	Ser	Pro	Leu	Leu	
				-20					-15					-10		
Thr	Leu	Ala	Leu	Leu	Gly	Gln	Cys	Ser	Leu	Phe	Xaa	Asn	Leu	Arg	Lys	
			-5				1				5					
Lys	Leu	Ala	Gly	Gln	Lys	Ala	Lys	Lys	Leu	Pro	Ser	Phe	Ser	Ser	Leu	
	10					15				20						
Pro	Leu	Thr	Leu	Trp	Pro	Leu	Thr	Pro	Gln	Phe	Ala	Glu	Leu	Thr	Thr	
25					30					35					40	
Val	Ala	Gln	Lys	Lys	Leu	Arg	Trp	Ser	Gly	Thr	Leu	Gly	Trp	Gly	Pro	
			45						50					55		
Val	Pro	Ser	Trp	Val	Gln	Phe	Phe	Leu	Gly							
			60					65								

<210> 426

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL
 <222> -30..-1

<400> 426

Met	Ala	Cys	Glu	Thr	His	Gly	Val	Leu	Val	Pro	Ala	His	Leu	Ser	Gly
-30					-25					-20					-15
Leu	Ile	Thr	Cys	Leu	Leu	Ala	Phe	Trp	Val	Pro	Ala	Ser	Cys	Ile	Gln
			-10					-5						1	
Arg	Cys	Ser	Gly	Ser	Pro	Leu	Pro	Leu							
	5						10								

<210> 427

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36..-1

<400> 427

Met	Ala	Pro	His	Thr	Ala	Ser	Phe	Gly	Val	Cys	Pro	Leu	Leu	Ser	Val
-35						-30				-25					
Thr	Arg	Val	Val	Ala	Thr	Glu	His	Trp	Leu	Phe	Leu	Ala	Ser	Leu	Ser
-20					-15				-10					-5	
Gly	Ile	Lys	Thr	Tyr	Gln	Ser	Tyr	Ile	Ser	Val	Phe	Cys	Lys	Val	Thr
			1					5					10		
Leu	Ile														

<210> 428

<211> 136

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18..-1

<220>

<221> UNSURE

<222> -2,73,102,107,110

<223> Xaa = any one of the twenty amino acids

<400> 428

Met	Asp	Ser	Leu	Arg	Lys	Met	Leu	Ile	Ser	Val	Ala	Met	Leu	Gly	Ala
			-15					-10					-5		
Xaa	Ala	Gly	Val	Gly	Tyr	Ala	Leu	Leu	Val	Ile	Val	Thr	Pro	Gly	Glu
	1				5					10					
Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg
15				20				25						30	
Ser	Arg	Glu	Glu	Ala	Arg	Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu	
			35				40					45			
Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp
		50					55					60			
Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Thr	Gly	Xaa	His	Arg	Glu	Thr	Gly
	65					70					75				
Leu	Ala	Ser	Val	Gly	Ala	Gly	Pro	Trp	Leu	Gly	Arg	Arg	Asn	Pro	Arg

80		85		90											
Gln	Leu	Ser	Pro	Ser	Trp	Ala	Xaa	Arg	Lys	Ile	Arg	Xaa	Glu	Asn	Xaa
95					100					105					110
Met	Pro	Gly	Leu	Ser	Gly	Val	Leu								
					115										

<210> 429
 <211> 194
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -65...-1

<220>
 <221> UNSURE
 <222> 20,83,95,121
 <223> Xaa = any one of the twenty amino acids

<400> 429

Met	Gln	Asp	Ala	Pro	Leu	Ser	Cys	Leu	Ser	Pro	Thr	Lys	Trp	Ser	Ser
-65					-60					-55					-50
Val	Ser	Ser	Ala	Asp	Ser	Thr	Glu	Lys	Ser	Ala	Ser	Ala	Ala	Gly	Thr
			-45					-40						-35	
Arg	Asn	Leu	Pro	Phe	Gln	Phe	Cys	Leu	Arg	Gln	Ala	Leu	Arg	Met	Lys
			-30				-25					-20			
Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr	Gly	Val	Glu
		-15				-10					-5				
Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile	Phe	Ser	Arg	Ala
1				5					10					15	
Gly	Leu	Asp	Asn	Xaa	Arg	Gly	Phe	Ser	Leu	Gly	Asn	Trp	Ile	Cys	Met
			20					25					30		
Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr	Ala	Gln	Thr	Val	Leu	Asp
		35				40						45			
Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe	Gln	Ile	Asn	Ser	Phe	Ala	Trp
	50					55					60				
Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu	Asn	Asn	His	Cys	His	Val	Ala	Cys
	65				70					75					
Ser	Ala	Leu	Xaa	Thr	Asp	Asp	Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Xaa
80				85					90						95
Lys	Ile	Val	Lys	Glu	Thr	Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys
			100					105					110		
Lys	His	Cys	Glu	Gly	Arg	Asp	Leu	Ser	Xaa	Trp	Lys	Lys	Gly	Cys	Glu
			115				120						125		
Val	Ser														

<210> 430
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<220>

<221> UNSURE
 <222> 27,29,38,42,43,50,55,60
 <223> Xaa = any one of the twenty amino acids

<400> 430

Met	Thr	Ser	Gln	Pro	Val	Pro	Asn	Glu	Thr	Ile	Ile	Val	Leu	Pro	Ser
				-65					-60					-55	
Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln
			-50					-45					-40		
Gly	Gln	Asp	Ser	Leu	Lys	Lys	His	Leu	His	Ala	Glu	Ile	Lys	Val	Ile
		-35					-30						-25		
Gly	Thr	Ile	Gln	Ile	Leu	Cys	Gly	Met	Met	Val	Leu	Ser	Leu	Gly	Ile
		-20				-15					-10				
Ile	Leu	Ala	Ser	Ala	Ser	Phe	Ser	Pro	Asn	Phe	Thr	Gln	Val	Thr	Ser
-5					1				5					10	
Thr	Leu	Leu	Asn	Ser	Ala	Tyr	Pro	Phe	Ile	Gly	Pro	Phe	Phe	Val	Xaa
			15					20					25		
Lys	Xaa	Ser	Glu	Glu	Gly	Arg	Met	Gly	Gln	Xaa	Gly	Glu	Glu	Xaa	Xaa
		30					35					40			
Asn	Ser	Leu	Asn	Phe	Pro	Xaa	Ala	Ser	Leu	Leu	Xaa	Leu	Ile	Cys	Gln
		45				50					55				
Xaa	Gln	Gly	Phe	Asn	Gly	Glu	Ser	Cys	Ser	Pro	Val	Gly			
60					65					70					

<210> 431
 <211> 248
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<220>
 <221> UNSURE
 <222> -25,65,79,83,90,91,94,106,112,130,131,155
 <223> Xaa = any one of the twenty amino acids

<400> 431

Met	Thr	Ser	Gln	Pro	Val	Pro	Asn	Glu	Thr	Ile	Ile	Val	Leu	Pro	Ser
				-65					-60					-55	
Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln
			-50					-45					-40		
Gly	Gln	Asp	Ser	Leu	Lys	Lys	His	Leu	His	Ala	Glu	Xaa	Lys	Val	Ile
		-35					-30						-25		
Gly	Thr	Ile	Gln	Ile	Leu	Cys	Gly	Met	Met	Val	Leu	Ser	Leu	Gly	Ile
		-20				-15					-10				
Ile	Leu	Ala	Ser	Ala	Ser	Phe	Ser	Pro	Asn	Phe	Thr	Gln	Val	Thr	Ser
-5					1				5					10	
Thr	Leu	Leu	Asn	Ser	Ala	Tyr	Pro	Phe	Ile	Gly	Pro	Phe	Phe	Phe	Ile
			15					20					25		
Ile	Ser	Gly	Ser	Leu	Ser	Ile	Ala	Thr	Lys	Lys	Arg	Leu	Thr	Asn	Leu
		30					35					40			
Leu	Val	His	Thr	Thr	Leu	Val	Gly	Ser	Ile	Leu	Ser	Ala	Leu	Ser	Ala
		45				50					55				
Leu	Val	Gly	Phe	Ile	Xaa	Leu	Ser	Val	Lys	Gln	Ala	Thr	Leu	Asn	Pro
60					65					70					75

Ala Ser Leu Xaa Cys Glu Leu Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa
80 85 90
Tyr Val Xaa Tyr Phe Tyr His Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr
95 100 105
Thr Ala Lys Ala Xaa Leu Ala Gly Thr Leu Ser Leu Met Leu Ile Cys
110 115 120
Thr Leu Leu Glu Phe Cys Xaa Xaa Val Leu Thr Ala Val Leu Arg Trp
125 130 135
Lys Gln Ala Tyr Ser Asp Phe Pro Gly Ser Val Leu Phe Leu Pro Xaa
140 145 150 155
Ser Tyr Ile Gly Asn Ser Gly Met Ser Ser Lys Met Thr His Asp Cys
160 165 170
Gly Tyr Glu Glu Leu Leu Thr Ser
175

<210> 432
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36...-1

<220>
<221> UNSURE
<222> -24,11
<223> Xaa = any one of the twenty amino acids

<400> 432
Met Gln Val Pro His Leu Arg Val Trp Thr Gln Val Xaa Asp Thr Phe
-35 -30 -25
Ile Gly Tyr Arg Asn Leu Gly Phe Thr Ser Met Cys Ile Leu Phe His
-20 -15 -10 -5
Cys Leu Leu Ser Phe Gln Val Phe Lys Lys Lys Arg Lys Leu Xaa Leu
1 5 10
Phe

<210> 433
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 433
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
-10 -5 1
Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser Ala
5 10 15
Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
20 25 30
Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
35 40 45 50
Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly

55
His Arg Ile Cys Asp Leu
70

60

65

<210> 434
<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -58...-1

<400> 434
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
-55 -50 -45
Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
-40 -35 -30
Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
-25 -20 -15
Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
-10 -5 1 5
Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
10 15 20
Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser Ala
25 30 35
Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu Asp
40 45 50
Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn Leu
55 60 65 70
Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg Ser
75 80 85

<210> 435
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<220>
<221> UNSURE
<222> 56,59,63,70,73,78,79,104,105
<223> Xaa = any one of the twenty amino acids

<400> 435
Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
-15 -10 -5
Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
1 5 10 15
Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
20 25 30
Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser
35 40 45
Glu Ser Pro Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro

50		55		60											
Val	Pro	Pro	Pro	Leu	Xaa	Asp	Leu	Xaa	Met	Thr	Pro	Arg	Xaa	Xaa	Arg
65				70					75						80
Ala	Trp	Gly	Pro	Val	Gly	Pro	Lys	Val	Pro	Pro	Ala	Val	Ser	Pro	Ala
			85					90						95	
Leu	Gly	Ser	Gly	Glu	His	Pro	Xaa	Xaa							
			100					105							

<210> 436
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<220>
 <221> UNSURE
 <222> 69,106,118,134,141
 <223> Xaa = any one of the twenty amino acids

<400> 436
Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
-15 -10 -5
Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
1 5 10 15
Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
20 25 30
Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys
35 40 45
Trp Ser Val Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro
50 55 60
Asn Asp Asn Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly
65 70 75 80
Val Ile Thr Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu
85 90 95
Thr Pro Gln Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln
100 105 110
Asp Pro Ser Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu
115 120 125
Pro Leu Cys Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln
130 135 140
Glu Gly
145

<210> 437
 <211> 110
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<220>
 <221> UNSURE

<222> -19,-3
 <223> Xaa = any one of the twenty amino acids

<400> 437

Met	Xaa	Leu	Met	Val	Leu	Val	Phe	Thr	Ile	Gly	Leu	Thr	Leu	Leu	Leu
-20					-15					-10					-5
Gly	Xaa	Gln	Ala	Met	Pro	Ala	Asn	Arg	Leu	Ser	Cys	Tyr	Arg	Lys	Ile
		1					5					10			
Leu	Lys	Asp	His	Asn	Cys	His	Asn	Leu	Pro	Glu	Gly	Val	Ala	Asp	Leu
	15						20					25			
Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp	Asp	Gly	Lys	Gly
	30					35					40				
Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Lys	Arg	Ile	Ala	Leu	Leu	Pro
45					50					55					60
Lys	Arg	Arg	Phe	Leu	Trp	Thr	Lys	Asp	Leu	Phe	Arg	Asp	Ser	Leu	Gln
			65						70					75	
Gln	Ser	Met	Arg	Ile	Phe	Met	Tyr	Ser	Gly	Glu	His	His	Ser		
			80					85					90		

<210> 438
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<220>
 <221> UNSURE
 <222> 43
 <223> Xaa = any one of the twenty amino acids

<400> 438

Met	Lys	Leu	Leu	Thr	His	Asn	Leu	Leu	Ser	Ser	His	Val	Arg	Gly	Val
-15					-10					-5					1
Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala	Thr	Glu	Val	Arg	Ile
		5					10					15			
Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala	Arg	Met	Ile	Pro	Lys
		20				25					30				
Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Xaa	Asp	Asn	Leu	Arg	Leu	Ile
	35					40					45				
Gln	Val	Pro	Arg	Arg	Ala	Gly									
50						55									

<210> 439
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<220>
 <221> UNSURE
 <222> 66

<223> Xaa = any one of the twenty amino acids

<400> 439

Met	Lys	Ser	Ala	Lys	Leu	Gly	Phe	Leu	Leu	Arg	Phe	Phe	Ile	Phe	Cys	
				-20					-15						-10	
Ser	Leu	Asn	Thr	Leu	Leu	Leu	Gly	Gly	Val	Asn	Lys	Ile	Ala	Glu	Lys	
			-5					1				5				
Ile	Cys	Gly	Asp	Leu	Lys	Asp	Pro	Cys	Lys	Leu	Asp	Met	Asn	Phe	Gly	
	10					15					20					
Ser	Cys	Tyr	Glu	Val	His	Phe	Arg	Tyr	Phe	Tyr	Asn	Arg	Thr	Ser	Lys	
25					30					35					40	
Arg	Cys	Glu	Thr	Phe	Val	Phe	Ser	Ser	Cys	Asn	Gly	Asn	Leu	Asn	Asn	
				45					50					55		
Phe	Lys	Leu	Lys	Ile	Glu	Arg	Glu	Val	Xaa	Cys	Val	Ala	Lys	Tyr	Lys	
			60					65					70			
Pro	Pro	Arg														
			75													

<210> 440

<211> 169

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<220>

<221> UNSURE

<222> 115

<223> Xaa = any one of the twenty amino acids

<400> 440

Met	Arg	Lys	Pro	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Leu	Leu	Lys	Val	Leu	
-25				-20					-15						-10	
Leu	Leu	Pro	Leu	Ala	Pro	Ala	Ala	Ala	Gln	Asp	Ser	Thr	Gln	Ala	Ser	
			-5					1				5				
Thr	Pro	Gly	Ser	Pro	Leu	Ser	Pro	Thr	Glu	Tyr	Gln	Arg	Phe	Phe	Ala	
		10				15						20				
Leu	Leu	Thr	Pro	Thr	Trp	Lys	Ala	Glu	Thr	Thr	Cys	Arg	Leu	Arg	Ala	
	25				30					35						
Thr	His	Gly	Cys	Arg	Asn	Pro	Thr	Leu	Val	Gln	Leu	Asp	Gln	Tyr	Glu	
40					45					50					55	
Asn	His	Gly	Leu	Val	Pro	Asp	Gly	Ala	Val	Cys	Ser	Asn	Leu	Pro	Tyr	
			60					65					70			
Ala	Ser	Trp	Phe	Glu	Ser	Phe	Cys	Gln	Phe	Thr	His	Tyr	Arg	Cys	Ser	
		75					80						85			
Asn	His	Val	Tyr	Tyr	Ala	Lys	Arg	Val	Leu	Cys	Ser	Gln	Pro	Val	Ser	
		90				95						100				
Ile	Leu	Ser	Pro	Asn	Thr	Leu	Lys	Glu	Ile	Glu	Xaa	Ser	Ala	Glu	Val	
	105					110					115					
Ser	Pro	Thr	Thr	Asp	Asp	Leu	Pro	His	Leu	Thr	Pro	Leu	His	Ser	Asp	
120					125					130					135	
Arg	Thr	Pro	Asp	Leu	Pro	Ala	Leu	Ala								
				140												

<210> 441

<211> 167
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -76..-1

<220>
 <221> UNSURE
 <222> 35,58,61,64
 <223> Xaa = any one of the twenty amino acids

<400> 441
 Met Gly Asp Tyr Leu Leu Arg Gly Tyr Arg Met Leu Gly Glu Thr Cys
 -75 -70 -65
 Ala Asp Cys Gly Thr Ile Leu Leu Gln Asp Lys Gln Arg Lys Ile Tyr
 -60 -55 -50 -45
 Cys Val Ala Cys Gln Glu Leu Asp Ser Asp Val Asp Lys Asp Asn Pro
 -40 -35 -30
 Ala Leu Asn Ala Gln Ala Ala Leu Ser Gln Ala Arg Glu His Gln Leu
 -25 -20 -15
 Ala Ser Ala Ser Glu Leu Pro Leu Gly Ser Arg Pro Ala Pro Gln Pro
 -10 -5 1
 Pro Val Pro Arg Pro Glu His Cys Glu Gly Ala Ala Ala Gly Leu Lys
 5 10 15 20
 Ala Ala Gln Gly Pro Pro Ala Pro Ala Val Pro Pro Asn Thr Xaa Val
 25 30 35
 Met Ala Cys Thr Gln Thr Ala Leu Leu Gln Lys Leu Thr Trp Ala Ser
 40 45 50
 Ala Glu Leu Gly Ser Xaa Thr Ser Xaa Gly Lys Xaa Ala Ser Ser Cys
 55 60 65
 Val Ala Leu Ser Ala His Val Arg Arg Pro Cys Ala Ala Cys Ser Ser
 70 75 80
 Tyr Ser Thr Lys Arg Ser Pro
 85 90

<210> 442
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<220>
 <221> UNSURE
 <222> 28,38,39,46,47,48,49,50
 <223> Xaa = any one of the twenty amino acids

<400> 442
 Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
 -15 -10 -5 1
 Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
 5 10 15
 Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Xaa Arg Thr Lys Tyr Glu

	20		25		30
Thr	Pro	Arg	Lys	Xaa	Xaa
	35		40		45
Xaa	Leu	Ser	Lys	Arg	Asp
50			55		

<210> 443
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<220>
 <221> UNSURE
 <222> -13,72,98,117,126,183,300
 <223> Xaa = any one of the twenty amino acids

<400> 443

Met	Ser	Trp	Thr	Val	Pro	Val	Val	Arg	Ala	Ser	Gln	Arg	Val	Ser	Ser
			-30					-25					-20		
Val	Gly	Ala	Asn	Xaa	Leu	Cys	Leu	Gly	Met	Ala	Leu	Cys	Pro	Arg	Gln
	-15					-10					-5				
Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	Thr	Pro	Val	Ser
1				5				10						15	
Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	Phe	Thr	Ser	Glu
			20					25					30		
Lys	Pro	Val	His	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val
			35				40						45		
Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu
	50					55						60			
Leu	Ala	Leu	Val	Asp	Leu	Asp	Glu	Xaa	Lys	Leu	Lys	Gly	Glu	Thr	Met
65					70					75					
Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro	Asn	Ile	Val	Cys
80					85				90						95
Ser	Lys	Xaa	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu	Val	Ile	Ile	Thr
			100					105					110		
Ala	Gly	Ala	Arg	Gln	Xaa	Lys	Gly	Glu	Thr	Arg	Leu	Asn	Leu	Xaa	Gln
			115				120						125		
Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser	Ile	Val	Gln	Tyr
	130						135					140			
Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro	Val	Asp	Ile	Leu
	145					150					155				
Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys	Asn	Arg	Ile	Ile
160					165					170				175	
Gly	Ser	Gly	Cys	Asn	Leu	Ile	Xaa	Ala	Arg	Phe	Arg	Phe	Leu	Ile	Gly
			180					185					190		
Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly	Trp	Ile	Leu	Gly
			195				200						205		
Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn	Ile	Ala
	210					215						220			
Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly	Thr	Asp	Lys	Asp
	225					230					235				
Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr	Ala	Thr	Ala	Tyr
240					245					250					255

Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser
 260 265 270
 Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His
 275 280 285
 Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile Xaa Glu Glu Val
 290 295 300
 Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu
 305 310 315
 Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser
 320 325 330 335
 Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu
 340 345

<210> 444
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 444
 Met Tyr Tyr Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His
 -10 -5 1
 Leu Pro Ile Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr
 5 10 15
 Val Tyr Pro Thr Ser Ala Gly
 20 25

<210> 445
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 445
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 -35 -30 -25
 Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
 -20 -15 -10
 Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met Pro
 -5 1 5 10
 Asp Asn

<210> 446
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<220>
 <221> UNSURE
 <222> 11,13,17
 <223> Xaa = any one of the twenty amino acids

<400> 446
 Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg Pro Leu Ala Ser
 -25 -20 -15
 Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser Gly Ser His Trp
 -10 -5 1 5
 Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser Leu Ser Ala Thr
 10 15 20
 Thr Arg Gly
 25

<210> 447
 <211> 242
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<220>
 <221> UNSURE
 <222> 100,103,122,161,182,184,185,200,207
 <223> Xaa = any one of the twenty amino acids

<400> 447
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 -30 -25 -20 -15
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 -10 -5 1
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 5 10 15
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 20 25 30
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 35 40 45 50
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 55 60 65
 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
 70 75 80
 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
 85 90 95
 Pro Xaa Glu Gly Xaa Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
 100 105 110
 Glu Lys Glu Ala Leu Val Pro Xaa Gln Lys Ala Thr Asp Ser Phe His
 115 120 125 130
 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
 135 140 145
 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Xaa Glu
 150 155 160
 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
 165 170 175
 His Lys Asp Xaa Leu Xaa Xaa Gly Thr Glu Ser Ser Ser His Ser Arg

180		185		190
Leu Ser Pro Arg Lys Xaa His Leu Leu Tyr Ile Leu Xaa Pro Ser Arg				
195	200		205	210
Gln Leu				

<210> 448
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 448	
Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu	
-60	-55 -50 -45
Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys	
	-40 -35 -30
Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu	
	-25 -20 -15
Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln	
	-10 -5 1
Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln	
5	10 15 20
Ala Leu Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu	
	25 30 35
Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met	
	40 45 50
Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe	
	55 60 65
Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln	
	70 75 80
Pro Glu Phe His Ile Glu Ile Leu Ser Ile	
85	90

<210> 449
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -61...-1

<220>
 <221> UNSURE
 <222> 13,28
 <223> Xaa = any one of the twenty amino acids

<400> 449	
Met Asn Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr	
-60	-55 -50
Glu Thr Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro	
-45	-40 -35 -30
Glu Ala Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala	
	-25 -20 -15

Leu Leu Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg
 -10 -5 1
 Pro Asp Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro
 5 10 15
 His Pro Cys Ala Thr Tyr Pro Pro Xaa
 20 25

<210> 450
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 450
 Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr
 -25 -20 -15
 Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro
 -10 -5 1 5
 Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile
 10 15 20
 Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly
 25 30 35
 Phe Asp Leu Asp Met Asp His Thr Ile
 40 45

<210> 451
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 451
 Met Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser
 -30 -25 -20
 Trp Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser
 -15 -10 -5
 Ser Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys
 1 5 10
 Ala Ile Ile Leu Met Lys
 15 20

<210> 452
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<220>

<221> UNSURE
 <222> 49,62,74,78
 <223> Xaa = any one of the twenty amino acids

<400> 452
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
 -35 -30 -25
 Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
 -20 -15 -10
 Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
 -5 1 5 10
 Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala Val Leu Trp
 15 20 25
 Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn Gln Trp Gln
 30 35 40
 His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser Ala Gln Ala
 45 50 55
 Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp Ile Pro Xaa
 60 65 70
 Leu Pro Gly Xaa Pro Gly Pro Pro Lys
 75 80

<210> 453
 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<220>
 <221> UNSURE
 <222> 49,80,116,120
 <223> Xaa = any one of the twenty amino acids

<400> 453
 Met Ser Thr Val Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile
 -35 -30 -25
 Cys Pro Ala Pro Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu
 -20 -15 -10
 Ser Pro Gly Ile Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp
 -5 1 5 10
 Tyr Pro Ala Leu Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe
 15 20 25
 Val Lys Gly His Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn
 30 35 40
 Cys Val Val Leu Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His
 45 50 55
 Gln Thr Arg Ser Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu
 60 65 70 75
 Gln Glu Lys Val Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His
 80 85 90
 Lys Glu Lys Arg Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg
 95 100 105
 Ala Lys Glu Thr Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu
 110 115 120

Ser Ser Lys Lys Val His
125

<210> 454
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26...-1

<220>
<221> UNSURE
<222> 88,107,111,117,121
<223> Xaa = any one of the twenty amino acids

<400> 454
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
40 45 50
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
55 60 65 70
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
75 80 85
Val Xaa Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
90 95 100
Gly Lys Met Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val
105 110 115
Glu Phe Xaa Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
120 125 130
Phe Asn Ile Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg
135 140 145 150
Arg Asn Trp Glu

<210> 455
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -64...-1

<400> 455
Met Thr Pro Arg Ile Leu Ser Glu Val Gln Phe Ser Ala Phe Cys Pro
-60 -55 -50
Tyr Trp Thr Ile Ala Arg Ile Leu Glu Arg Val Gly Ser Ala Cys Phe
-45 -40 -35
Arg Leu Glu Leu Cys Ala Ala Ile Val Gly Tyr Phe Val Leu Asp Val

-30 -25 -20
 Arg Thr Phe Leu Phe Ile Val Val Cys Val Ile Cys Val Thr Leu Asn
 -15 -10 -5
 Phe Pro Arg Phe Tyr Phe Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly
 1 5 10 15
 Thr Pro Pro Ile Gly Val His Ile Pro Ser Pro
 20 25

<210> 456
 <211> 257
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<220>
 <221> UNSURE
 <222> -8,100,101,143,153,156,182,184,188,192,199,202,203,214,229,230,233,234
 <223> Xaa = any one of the twenty amino acids

<400> 456
 Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
 -20 -15 -10
 Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
 -5 1 5
 Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
 10 15 20 25
 Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
 30 35 40
 Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
 45 50 55
 Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
 60 65 70
 Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
 75 80 85
 Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg
 90 95 100 105
 Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly
 110 115 120
 Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
 125 130 135
 Asn His Glu Ala Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa
 140 145 150
 Leu Glu Xaa Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
 155 160 165
 Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val
 170 175 180 185
 Ser Pro Xaa Asn Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro
 190 195 200
 Xaa Xaa Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly
 205 210 215
 Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa
 220 225 230
 Xaa

<210> 457
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60..-1

<220>
 <221> UNSURE
 <222> 11,51,53,69,75,83,85
 <223> Xaa = any one of the twenty amino acids

<400> 457
 Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
 -60 -55 -50 -45
 Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro
 -40 -35 -30
 Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu
 -25 -20 -15
 Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro
 -10 -5 1
 Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala Pro
 5 10 15 20
 Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg Ala
 25 30 35
 Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa Thr
 40 45 50
 Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile Val
 55 60 65
 Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa Phe
 70 75 80
 Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val Leu
 85 90 95 100
 Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr His
 105 110 115
 Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro Trp
 120 125 130
 Glu

<210> 458
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<220>
 <221> UNSURE
 <222> 40
 <223> Xaa = any one of the twenty amino acids

<400> 458
 Met Val Leu Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg

			-25					-20					-15				
Phe	Leu	Ser	Leu	Ser	Ala	Ala	Asp	Gly	Ser	Asp	Gly	Ser	His	Asp	Ser		
			-10					-5					1				
Trp	Asp	Val	Glu	Arg	Val	Ala	Glu	Trp	Pro	Trp	Leu	Ser	Gly	Thr	Ile		
5					10					15					20		
Arg	Ala	Val	Ser	His	Thr	Asp	Val	Thr	Lys	Lys	Asp	Leu	Lys	Val	Cys		
				25					30					35			
Val	Glu	Phe	Xaa	Gly	Glu	Ser	Trp	Arg	Lys	Arg	Arg	Trp	Ile	Glu	Val		
			40						45				50				
Tyr	Ser	Leu	Leu	Arg	Lys	Ala	Phe	Leu	Val	Lys	His	Asn	Leu	Val	Leu		
		55					60					65					
Ala	Glu	Arg	Lys	Ser	Pro	Glu	Ile	Ser	Trp	Gly							
	70					75											

<210> 459
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<220>
 <221> UNSURE
 <222> 63,69
 <223> Xaa = any one of the twenty amino acids

<400>	459																
Met	Leu	Val	Leu	Arg	Ser	Ala	Leu	Thr	Arg	Ala	Leu	Ala	Ser	Arg	Thr		
			-10					-5					1				
Leu	Ala	Pro	Gln	Met	Cys	Ser	Ser	Phe	Ala	Thr	Gly	Pro	Arg	Gln	Tyr		
5					10						15						
Asp	Gly	Ile	Phe	Tyr	Glu	Phe	Arg	Ser	Tyr	Tyr	Leu	Lys	Pro	Ser	Lys		
20					25					30					35		
Met	Asn	Glu	Phe	Leu	Glu	Asn	Phe	Glu	Lys	Asn	Ala	Gln	Leu	Arg	Thr		
				40					45					50			
Ala	His	Ser	Glu	Leu	Val	Gly	Tyr	Trp	Ser	Val	Xaa	Phe	Gly	Gly	Arg		
			55					60					65				
Met	Xaa	Thr	Val	Phe	His	Ile	Trp	Lys	Tyr	Asp	Asn	Phe	Ala	His	Arg		
		70				75						80					
Thr	Glu	Phe	Gln	Lys	Ala	Leu	Ala	Lys	Asp	Lys	Glu	Trp	Gln	Glu	Gln		
	85					90					95						
Phe	Leu	Ile	Pro	Asn	Leu	Ala	Leu	Asn									
100					105												

<210> 460
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 460
 Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp

-15 -10 -5
 Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
 1 5 10 15
 Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Ile
 20 25

<210> 461
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<220>
 <221> UNSURE
 <222> 18,79,90,93
 <223> Xaa = any one of the twenty amino acids

<400> 461
 Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys
 -10 -5 1
 Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro
 5 10 15
 Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro
 20 25 30 35
 Thr Val Tyr Ser Ser Ala Pro Phe His Ala Pro Leu Pro Val Gln Asn
 40 45 50
 Ser Leu Trp Gly His Pro Leu His Gly Cys Ser Trp Gln Cys His His
 55 60 65
 Pro Gln Gly Gln Asn Leu Gln Pro Ala Ser Leu Xaa Thr His Leu Ser
 70 75 80
 Lys Pro Lys Arg His Phe Xaa Lys Lys Xaa Cys Gln Ala
 85 90 95

<210> 462
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

<400> 462
 Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala
 -40 -35 -30
 Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile
 -25 -20 -15 -10
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu
 -5 1 5
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp
 10 15 20
 Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu
 25 30 35
 Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His Lys Thr Val Val Asn

40		45		50		55									
Gly	Lys	Glu	Cys	Ile	Asn	Phe	Ala	Ser	Phe	Asn	Phe	Leu	Gly	Leu	Leu
				60					65					70	
Asp	Asn	Pro	Arg	Val	Lys	Ala	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Lys	Tyr
			75					80					85		
Gly	Val	Gly	Thr	Cys	Gly	Pro	Cys	Gly	Phe	Tyr	Gly	Thr	Phe	Glu	
	90						95					100			

<210> 463
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<220>
 <221> UNSURE
 <222> 2,3,58,61
 <223> Xaa = any one of the twenty amino acids

<400> 463
Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
-30 -25 -20 -15
Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Xaa
-10 -5 1
Xaa Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
5 10 15
Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
20 25 30
Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
35 40 45 50
Thr Leu Arg Ile Asp Val Leu Xaa Pro Glu Xaa Leu Lys Ser Glu Ser
55 60 65
Ala Lys Glu Pro Pro Gly Tyr Asn Ser Leu Pro Leu Lys Leu Leu Gly
70 75 80
Thr Gly Lys Ala Ile Thr Lys Leu Phe Ile Ser Val Phe Arg Thr Lys
85 90 95
Lys Glu Arg Lys Glu Ser Thr Met Glu Glu Lys Lys Glu Leu Thr Val
100 105 110
Glu Lys Lys Arg Thr Pro Arg Met Glu Glu Arg Lys Glu Leu Ile Val
115 120 125 130
Glu Lys Lys Lys Arg Lys Glu Ser Thr Glu Lys Thr Lys Leu Thr Lys
135 140 145
Glu Glu Lys Lys Gly Lys Lys Leu Thr Lys Lys Ser Thr Lys Val Val
150 155 160
Lys Lys Leu Cys Lys Val Tyr Arg Glu Gln His Ser Arg Ser Tyr Asp
165 170 175
Ser Ile Glu Thr Thr Ser Thr Thr Val Leu Leu Ala Gln Thr Pro Leu
180 185 190
Val Lys Cys Lys Phe Leu Tyr Asn
195 200

<210> 464
 <211> 61
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 464

Met	Thr	Phe	Arg	His	Gln	Asp	Asn	Ser	Leu	Met	Phe	Phe	Ser	Met	Met
	-20					-15					-10				
Ala	Thr	Cys	Thr	Ser	Asn	Val	Gly	Phe	Thr	His	Thr	Thr	Met	Asn	Cys
-5					1				5					10	
Ser	Leu	Thr	Ser	Pro	Val	Asp	Phe	Lys	Asp	Leu	Leu	Arg	Val	Leu	Leu
			15					20					25		
Ile	Lys	Phe	Gly	Tyr	Asp	Arg	Lys	Ser	Thr	Ile	Lys	Ser			
		30					35					40			

<210> 465

<211> 34

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<220>

<221> UNSURE

<222> 11

<223> Xaa = any one of the twenty amino acids

<400> 465

Met	Phe	Leu	Lys	Ser	Gly	Ala	Gly	Leu	Ser	Ser	Cys	Leu	Leu	Pro	Leu
				-15				-10						-5	
Cys	Trp	Leu	Glu	Arg	Lys	Asp	His	Gly	Arg	Arg	Pro	Ser	Xaa	His	Pro
			1					5				10			
Gly	Arg														
			15												

<210> 466

<211> 215

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -54...-1

<220>

<221> UNSURE

<222> -52,-45,-42,-39,27,97,104,124,127

<223> Xaa = any one of the twenty amino acids

<400> 466

Met	Asn	Xaa	Tyr	Ala	Ser	Pro	Phe	Asn	Xaa	Gln	Leu	Xaa	Tyr	Leu	Xaa
				-50					-45					-40	
Leu	Ser	Arg	Phe	Glu	Cys	Val	His	Arg	Asp	Gly	Arg	Val	Ile	Thr	Leu
			-35					-30					-25		

Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
 -20 -15 -10
 Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
 -5 1 5 10
 Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
 15 20 25
 Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
 30 35 40
 Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
 45 50 55
 Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
 60 65 70
 Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
 75 80 85 90
 Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
 95 100 105
 Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
 110 115 120
 Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
 125 130 135
 Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
 140 145 150
 Ile Ile Arg Lys Cys Phe Ile
 155 160

<210> 467
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 467
 Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr Ser Lys Arg
 -15 -10 -5
 Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
 1 5 10

<210> 468
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<220>
 <221> UNSURE
 <222> 56
 <223> Xaa = any one of the twenty amino acids

<400> 468
 Met Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu
 -20 -15 -10

Phe Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys
 -5 1 5
 Phe Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser
 10 15 20
 Leu Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe
 25 30 35 40
 Pro Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa
 45 50 55
 Tyr Trp Asp Asn Leu
 60

<210> 469
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 469
 Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 470
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43..-1

<220>
 <221> UNSURE
 <222> 15
 <223> Xaa = any one of the twenty amino acids

<400> 470
 Met Thr Pro Gln Tyr Leu Pro His Gly Gly Lys Tyr Gln Val Leu Gly
 -40 -35 -30
 Asp Tyr Ser Leu Ala Val Val Phe Pro Leu His Phe Ser Asp Leu Ile
 -25 -20 -15
 Ser Val Leu Tyr Leu Ile Pro Lys Thr Leu Thr Thr Asn Thr Ala Val
 -10 -5 1 5
 Lys His Ser Ile Gln Lys Asn Cys Met Xaa Leu Val Leu Gly Lys Leu
 10 15 20
 Leu Ser Gln

<210> 471
 <211> 63

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 471
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
-15 -10 -5 1
Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
5 10 15
Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
20 25 30
Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr Ser Ser Ala
35 40 45

<210> 472
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -58...-1

<220>
<221> UNSURE
<222> 54,55,56,74,76,89,103
<223> Xaa = any one of the twenty amino acids

<400> 472
Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
-55 -50 -45
Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
-40 -35 -30
Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
-25 -20 -15
Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
-10 -5 1 5
Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
10 15 20
Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile
25 30 35
Tyr Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa
40 45 50
Xaa Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser
55 60 65 70
His Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro
75 80 85
Thr Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys
90 95 100
Xaa Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly
105 110 115
Gln Val Asn
120

<210> 473
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -71..-1

<220>
 <221> UNSURE
 <222> -70,-69
 <223> Xaa = any one of the twenty amino acids

<400> 473
 Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
 -70 -65 -60
 Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
 -55 -50 -45 -40
 Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
 -35 -30 -25
 Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu Leu
 -20 -15 -10
 Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His Gln
 -5 1 5
 Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr Trp
 10 15 20 25
 Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu His
 30 35 40
 Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu Ala
 45 50 55
 Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro Asp
 60 65 70
 Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser Leu
 75 80 85
 Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly Ile
 90 95 100 105
 Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala Ala
 110 115 120
 Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe Glu
 125 130 135
 Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr Val Gly Ile
 140 145 150
 Glu Asn Arg Thr Leu Tyr Phe Phe Leu Lys Arg Leu Leu Arg
 155 160 165

<210> 474
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<220>
 <221> UNSURE

<222> 24,30,42,77,82,95

<223> Xaa = any one of the twenty amino acids

<400> 474

Met	Glu	Arg	Gln	Ser	Arg	Val	Met	Ser	Glu	Lys	Asp	Glu	Tyr	Gln	Phe	
	-35					-30					-25					
Gln	His	Gln	Gly	Ala	Val	Glu	Leu	Leu	Val	Phe	Asn	Phe	Leu	Leu	Ile	
	-20					-15				-10						
Leu	Thr	Ile	Leu	Thr	Ile	Trp	Leu	Phe	Lys	Asn	His	Arg	Phe	Arg	Phe	
	-5				1				5					10		
Leu	His	Glu	Thr	Gly	Gly	Ala	Met	Val	Tyr	Gly	Leu	Xaa	Met	Gly	Leu	
		15					20					25				
Ile	Leu	Xaa	Tyr	Ala	Thr	Ala	Pro	Thr	Asp	Ile	Glu	Ser	Gly	Xaa	Val	
	30					35					40					
Tyr	Asp	Cys	Val	Lys	Leu	Thr	Phe	Ser	Pro	Ser	Thr	Leu	Leu	Val	Asn	
	45					50					55					
Ile	Thr	Asp	Gln	Val	Tyr	Glu	Tyr	Lys	Tyr	Lys	Arg	Glu	Ile	Ser	Gln	
60					65					70					75	
His	Xaa	Ile	Asn	Pro	His	Xaa	Gly	Asn	Ala	Ile	Leu	Glu	Lys	Met	Thr	
			80					85						90		
Phe	Asp	Pro	Xaa	Ile	Phe	Phe	Asn	Val	Leu	Leu	Pro	Pro	Ile	Ile	Phe	
		95						100					105			
His	Ala	Gly	Tyr	Ser	Leu	Lys	Lys	Arg	His	Phe	Phe	Gln	Asn	Leu	Gly	
		110					115					120				
Ser	Ile	Leu	Thr	Tyr	Ala	Phe	Leu	Gly	Thr	Ala	Ile	Ser	Cys	Ile	Val	
	125					130					135					
Ile	Gly															
140																

<210> 475

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<220>

<221> UNSURE

<222> 46,64

<223> Xaa = any one of the twenty amino acids

<400> 475

Met	Ser	Met	Gln	Phe	Leu	Phe	Lys	Met	Val	Ala	Leu	Cys	Cys	Cys	Leu	
	-20					-15				-10						
Trp	Lys	Ile	Ser	Gly	Cys	Glu	Glu	Val	Pro	Leu	Thr	Tyr	Asn	Leu	Leu	
	-5				1			5					10			
Lys	Cys	Leu	Leu	Asp	Lys	Ala	His	Cys	Val	Leu	Leu	Thr	Pro	Cys	Gly	
		15					20					25				
Tyr	Ile	Phe	Ser	Leu	Ile	Ser	Pro	Glu	Ile	Leu	Lys	Leu	Thr	Leu	Ile	
	30					35						40				
Thr	Leu	Xaa	Ile	Leu	Leu	Ile	Leu	Lys	Asn	Leu	His	Leu	Leu	Trp	Leu	
	45					50					55					
Thr	Val	Ser	Ser	Xaa	Cys	Val	His	Arg	Ser	Ser	Ala	Arg	Lys	Glu	Lys	
60					65					70					75	

<210> 476
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 476
 Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile Leu Leu Leu
 -20 -15 -10
 His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu Gly Tyr Lys
 -5 1 5
 Val Leu Gly Val Phe Phe Pro Ile Leu
 10 15

<210> 477
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<220>
 <221> UNSURE
 <222> -25,-2,4,83
 <223> Xaa = any one of the twenty amino acids

<400> 477
 Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
 -25 -20 -15
 Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His
 -10 -5 1 5
 Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
 10 15 20
 Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
 25 30 35
 Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys
 40 45 50
 Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys
 55 60 65
 Pro Arg Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr
 70 75 80 85
 Ser

<210> 478
 <211> 250
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<220>
 <221> UNSURE
 <222> 52,89,90,97,99
 <223> Xaa = any one of the twenty amino acids

<400> 478

Met	Arg	Ile	Leu	Gln	Leu	Ile	Leu	Leu	Ala	Leu	Ala	Thr	Gly	Leu	Val
			-15					-10					-5		
Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	His	Ser
	1				5				10						
Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	Leu	Cys	Gly
15				20					25						30
Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	Ala	His	Cys	Leu
				35				40						45	
Lys	Pro	Arg	Tyr	Ile	Xaa	His	Leu	Gly	Gln	His	Asn	Leu	Gln	Lys	Glu
			50					55					60		
Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	Glu	Ser	Phe	Pro	His	Pro
	65					70						75			
Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	Asp	Xaa	Xaa	Asn	Asp	Ile	Met
	80				85					90					
Leu	Val	Xaa	Met	Xaa	Ser	Pro	Val	Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro
95					100					105					110
Leu	Thr	Leu	Ser	Ser	Arg	Cys	Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile
				115					120					125	
Ser	Gly	Trp	Gly	Ser	Thr	Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr
			130					135					140		
Leu	Arg	Cys	Ala	Asn	Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn
	145						150					155			
Ala	Tyr	Pro	Gly	Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln
	160					165				170					
Glu	Gly	Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
175					180				185						190
Cys	Asn	Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys
			195					200					205		
Ala	Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val
		210						215					220		
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
		225					230								

<210> 479
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 479

Met	Ala	Ala	Ser	Thr	Ser	Met	Val	Pro	Val	Ala	Val	Thr	Ala	Ala	Val
	-20					-15				-10					
Ala	Pro	Val	Leu	Ser	Ile	Asn	Ser	Asp	Phe	Ser	Asp	Leu	Arg	Glu	Ile
-5				1				5					10		
Lys	Lys	Gln	Leu	Leu	Ile	Ala	Gly	Leu	Thr	Arg	Glu	Arg	Gly	Leu	
		15				20					25				
Leu	His	Ser	Ser	Lys	Trp	Ser	Ala	Glu	Leu	Ala	Phe	Ser	Leu	Pro	Ala
		30				35					40				

Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
 45 50 55
 Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
 60 65 70 75
 Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
 80 85 90
 Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
 95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 480
 <211> 239
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<220>
 <221> UNSURE
 <222> 20,98,99,100,101,103,150,151,152,173
 <223> Xaa = any one of the twenty amino acids

<400> 480
 Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
 -25 -20 -15 -10
 Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
 -5 1 5
 Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
 10 15 20
 Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
 25 30 35
 Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
 40 45 50 55
 Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
 60 65 70
 Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
 75 80 85
 Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
 90 95 100
 Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
 105 110 115
 Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
 120 125 130 135
 Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
 140 145 150
 Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
 155 160 165
 Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
 170 175 180
 Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln
 185 190 195
 Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser

200

205

210

<210> 481

<211> 208

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -92..-1

<220>

<221> UNSURE

<222> -79,-78,-76,22,36,46,51,57,70,73,74,111

<223> Xaa = any one of the twenty amino acids

<400> 481

Met	Arg	Glu	Pro	Gln	Lys	Arg	Thr	Ala	Thr	Ile	Ala	Lys	Xaa	Xaa	Ala
		-90				-85						-80			
Xaa	Glu	Gly	Leu	Arg	Asp	Pro	Tyr	Gly	Arg	Leu	Cys	Gly	Ser	Glu	His
	-75				-70						-65				
Pro	Arg	Arg	Pro	Pro	Glu	Arg	Pro	Glu	Glu	Asp	Pro	Ser	Thr	Pro	Glu
-60				-55					-50						-45
Glu	Ala	Ser	Thr	Thr	Pro	Glu	Glu	Ala	Ser	Ser	Thr	Ala	Gln	Ala	Gln
			-40					-35					-30		
Lys	Pro	Ser	Val	Pro	Arg	Ser	Asn	Phe	Gln	Gly	Thr	Lys	Lys	Ser	Leu
		-25				-20						-15			
Leu	Met	Ser	Ile	Leu	Ala	Leu	Ile	Phe	Ile	Met	Gly	Asn	Ser	Ala	Lys
	-10				-5						1				
Glu	Ala	Leu	Val	Trp	Lys	Val	Leu	Gly	Lys	Leu	Gly	Met	Gln	Pro	Gly
5				10				15						20	
Arg	Xaa	His	Ser	Ile	Phe	Gly	Asp	Pro	Lys	Lys	Ile	Val	Thr	Glu	Xaa
		25				30						35			
Phe	Val	Arg	Arg	Gly	Tyr	Leu	Ile	Tyr	Xaa	Pro	Val	Pro	Arg	Xaa	Ser
		40				45					50				
Pro	Val	Glu	Tyr	Xaa	Phe	Phe	Trp	Gly	Pro	Arg	Ala	His	Val	Glu	Ser
	55				60			65							
Ser	Xaa	Leu	Lys	Xaa	Xaa	His	Phe	Val	Ala	Arg	Val	Arg	Asn	Arg	Cys
	70				75			80							
Ser	Lys	Asp	Trp	Pro	Cys	Asn	Tyr	Asp	Trp	Asp	Ser	Asp	Asp	Asp	Ala
85				90				95						100	
Glu	Val	Glu	Ala	Ile	Leu	Asn	Ser	Gly	Ala	Xaa	Gly	Tyr	Ser	Ala	Pro
			105					110						115	

<210> 482

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39..-1

<220>

<221> UNSURE

<222> -32,-31

<223> Xaa = any one of the twenty amino acids

<400> 482

Met	Asn	Val	Gly	Thr	Ala	His	Xaa	Xaa	Val	Asn	Pro	Asn	Thr	Arg	Val
				-35					-30					-25	
Met	Asn	Ser	Arg	Gly	Ile	Trp	Leu	Ser	Tyr	Val	Leu	Ala	Ile	Gly	Leu
			-20					-15					-10		
Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val
		-5					1				5				
Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu
10					15					20					25
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala
				30					35					40	
Arg	Leu	Leu	Thr	His	Trp										
				45											

<210> 483

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 483

Met	Arg	Thr	Leu	Phe	Gly	Ala	Val	Arg	Ala	Pro	Phe	Ser	Ser	Leu	Thr
		-25					-20					-15			
Leu	Leu	Leu	Ile	Thr	Pro	Ser	Pro	Ser	Pro	Leu	Leu	Phe	Asp	Arg	Gly
		-10				-5					1				5
Leu	Ser	Leu	Arg	Ser	Ala	Met	Ser								
				10											

<210> 484

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<220>

<221> UNSURE

<222> 41,44

<223> Xaa = any one of the twenty amino acids

<400> 484

Met	Leu	Gly	Phe	Phe	Leu	Phe	Leu	Ser	Phe	Val	Leu	Met	Tyr	Asp	Gly
		-15				-10					-5				
Leu	Arg	Leu	Phe	Gly	Ile	Leu	Ser	Thr	Cys	Arg	Val	His	His	Thr	Met
1				5					10					15	
Asn	Gln	Phe	Leu	Ile	Asp	Ile	Ser	Ser	Phe	Thr	Ser	Arg	Val	Lys	Lys
			20				25						30		
Lys	Ile	Phe	Leu	Phe	Tyr	Ala	Phe	Xaa	Gly	Cys	Xaa	Phe	Gln	Ser	Ala
		35					40					45			
Thr															

<210> 485
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55..-1

<220>
 <221> UNSURE
 <222> -48,-47,-46,-39,-23,-22,17,41,42
 <223> Xaa = any one of the twenty amino acids

<400> 485
 Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu
 -55 -50 -45 -40
 Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
 -35 -30 -25
 Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 -20 -15 -10
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
 -5 1 5
 Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val
 10 15 20 25
 Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Xaa
 30 35 40
 Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu Gly Arg
 45 50 55
 Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln Gly Trp
 60 65 70
 Ala Leu
 75

<210> 486
 <211> 209
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -84..-1

<220>
 <221> UNSURE
 <222> 48,50,74,76
 <223> Xaa = any one of the twenty amino acids

<400> 486
 Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu
 -80 -75 -70
 Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr
 -65 -60 -55
 Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly
 -50 -45 -40
 Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu
 -35 -30 -25

Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu
 -20 -15 -10 -5
 Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr
 1 5 10
 Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly
 15 20 25
 Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val
 30 35 40
 Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala Ala Leu His
 45 50 55 60
 Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Xaa Val Xaa
 65 70 75
 Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg
 80 85 90
 Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr
 95 100 105
 Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser
 110 115 120
 His
 125

<210> 487
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 487
 Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
 -15 -10 -5
 Ala His Pro Pro Gln Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp
 1 5 10 15
 Val Gly Ile Cys

<210> 488
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 488
 Met Met Ser Ser Glu Leu Arg Arg Asn Pro His Phe Leu Lys Ser Asn
 -25 -20 -15
 Leu Phe Leu Gln Leu Leu Val Ser His Glu Ile Val Cys Ala Thr Glu
 -10 -5 1
 Thr Val Thr Thr Asn Phe Leu Arg His Glu Lys Ala
 5 10 15

<210> 489
 <211> 163
 <212> PRT

<210> 491
 <211> 218
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -50..-1

<220>
 <221> UNSURE
 <222> 44,47,58,91,99,100,107,113,116,132,134,135,140,159
 <223> Xaa = any one of the twenty amino acids

<400> 491
 Met His His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
 -50 -45 -40 -35
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
 -30 -25 -20
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
 -15 -10 -5
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
 1 5 10
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys Tyr Ala Val Ser Ser
 15 20 25 30
 Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Xaa Lys Gln
 35 40 45
 Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro Xaa Gln Asp Leu Lys
 50 55 60
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys Gly Ser Glu Asn Ser
 65 70 75
 Gln Pro Glu Glu Met Ser Gln Glu Pro Glu Ile Asn Xaa Gly Gly Asp
 80 85 90
 Arg Lys Val Glu Xaa Xaa Met Lys Lys His Gly Ser Xaa His Met Gly
 95 100 105 110
 Phe Pro Xaa Asn Leu Xaa Asn Gly Ala Thr Ala Asp Asn Gly Asp Asp
 115 120 125
 Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro Glu Ser Xaa Gln Phe
 130 135 140
 Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp Phe Ser Gly His Pro
 145 150 155
 Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln
 160 165

<210> 492
 <211> 216
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<220>
 <221> UNSURE

<222> 72,74,77,82,92,105,115,124
 <223> Xaa = any one of the twenty amino acids

<400> 492

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Met Val Cys Val Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val
-15          -10          -5          1
Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr
      5          10          15
Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His
      20          25          30
Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser
      35          40          45
Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys
50          55          60          65
Ile Asn Ser Phe Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met
      70          75          80
Xaa Thr Lys Tyr Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln
      85          90          95
Gln Ser Trp Pro Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu
      100          105          110
Ser Xaa Pro Leu Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn
      115          120          125
Gly Pro Gly Thr Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly
130          135          140          145
Ile Leu Gly Ile Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys
      150          155          160
Arg Val Lys Thr Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser
      165          170          175
Asn Tyr Phe Ile Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys
      180          185          190
Ser Val Tyr Leu Gly Arg Ile Val
      195          200

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<210> 493

<211> 134

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<220>

<221> UNSURE

<222> 25,55

<223> Xaa = any one of the twenty amino acids

<400> 493

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Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly
      -15          -10          -5
Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr
      1          5          10
Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu Ala
      15          20          25
Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile
30          35          40          45
Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile Pro

```

				50					55				60				
Val	Ser	Gly	Ser	Lys	Ser	Glu	Gly	Leu	Leu	Tyr	Val	His	Ser	Ser	Arg		
			65					70					75				
Gly	Gly	Pro	Phe	Gln	Arg	Trp	His	Leu	Asp	Glu	Val	Phe	Leu	Glu	Leu		
		80					85					90					
Lys	Asp	Gly	Gln	Gln	Ile	Pro	Val	Phe	Lys	Leu	Ser	Gly	Glu	Asn	Gly		
	95					100					105						
Asp	Glu	Val	Lys	Lys	Glu												
110					115												

<210> 494
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<220>
 <221> UNSURE
 <222> -8,53,57
 <223> Xaa = any one of the twenty amino acids

Met	Ala	Val	Thr	Ala	Leu	Ala	Ala	Xaa	Thr	Trp	Leu	Gly	Val	Trp	Gly		
	-15					-10					-5						
Val	Arg	Thr	Met	Gln	Ala	Arg	Gly	Phe	Gly	Ser	Asp	Gln	Ser	Glu	Asn		
1			5				10					15					
Val	Asp	Arg	Gly	Ala	Gly	Ser	Ile	Arg	Glu	Ala	Gly	Gly	Ala	Phe	Gly		
		20					25					30					
Lys	Arg	Glu	Gln	Ala	Glu	Glu	Glu	Arg	Tyr	Phe	Arg	Ala	Gln	Ser	Thr		
	35					40					45						
Glu	Gln	Leu	Ala	Xaa	Leu	Lys	Lys	Xaa	His	Glu	Glu	Glu	Ile	Val	His		
	50				55					60							
His	Arg	Glu	Gly	Asp													
65																	

<210> 495
 <211> 292
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<220>
 <221> UNSURE
 <222> 62,82,85,95,112,186,212,244
 <223> Xaa = any one of the twenty amino acids

Met	His	Gly	Leu	Leu	His	Tyr	Leu	Phe	His	Thr	Arg	Asn	His	Thr	Phe		
			-25					-20					-15				
Ile	Val	Leu	His	Leu	Val	Leu	Gln	Gly	Met	Val	Tyr	Thr	Glu	Tyr	Thr		
		-10					-5					1					

Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr
 5 10 15
 Leu Leu Leu Pro Tyr Leu Leu Gly Val Asn Leu Phe Phe Phe Thr
 20 25 30 35
 Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu
 40 45 50
 Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe Pro Lys Asn
 55 60 65
 Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Xaa His
 70 75 80
 Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His His Cys Val
 85 90 95
 Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa Phe Leu Ile
 100 105 110 115
 Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser
 120 125 130
 Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu
 135 140 145
 Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp Thr Val Phe
 150 155 160
 Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu
 165 170 175
 Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr Leu Leu Phe
 180 185 190 195
 Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg
 200 205 210
 Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro
 215 220 225
 Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His Gly Leu Arg
 230 235 240
 Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg
 245 250 255
 Lys Lys Gln Glu
 260

<210> 496

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -56..-1

<220>

<221> UNSURE

<222> 5,10,19,33

<223> Xaa = any one of the twenty amino acids

<400> 496

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
 -55 -50 -45
 Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Asn Pro Ser
 -40 -35 -30 -25
 Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
 -20 -15 -10
 Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu Thr Gly

	-5						1				5								
Pro	Xaa	Thr	Asp	Gly	Ile	Pro	Phe	Ala	Leu	Xaa	Ser	Ala	Ala	Gly	Pro				
10						15					20								
Phe	Cys	Ala	Ser	Phe	Pro	Ser	Gly	Xaa	Leu	Ser	Pro	Pro	Gly	Pro	Leu				
25					30					35					40				
Pro	Gly	Val	Arg	Gly	Leu	Pro	Leu	Pro	Ser	Val	Phe	Tyr	Ser	Cys	Gly				
				45					50					55					
Ala	His	Pro	Lys	Val	Leu	Lys	Val	Ala	Leu										
			60					65											

<210> 497
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<220>
 <221> UNSURE
 <222> -26,-19,-2
 <223> Xaa = any one of the twenty amino acids

<400>	497																		
Met	Leu	Xaa	Leu	Ser	Arg	Ala	Thr	Lys	Xaa	Gly	Arg	Ala	Arg	Trp	Leu				
			-25					-20					-15						
Met	Pro	Val	Ile	Pro	Ala	Leu	Gln	Glu	Ala	Xaa	Ala	Gly	Gly	Ser	Arg				
		-10					-5					1							
Gly	Gln	Glu	Phe	Glu	Thr	Ser	Leu	Ala	Asn	Met	Glu	Thr	Glu	Ala	Gly				
5					10				15					20					
Glu	Leu	Leu	Lys	Pro	Arg	Arg	Arg	Arg	Leu	Gln									
			25					30											

<210> 498
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<220>
 <221> UNSURE
 <222> 77
 <223> Xaa = any one of the twenty amino acids

<400>	498																		
Met	His	Leu	Leu	Ser	Asn	Trp	Ala	Asn	Pro	Ala	Ser	Ser	Arg	Arg	Pro				
			-10					-5					1						
Ser	Met	Ala	Ala	Ser	Gly	Thr	Ser	Trp	Ile	Ser	Ser	Thr	Leu	Ala	His				
	5				10						15								
Ser	Leu	Ser	Leu	Arg	Asp	Val	Ser	Glu	Arg	Leu	Cys	Ser	Cys	Trp	Arg				
20				25					30					35					
Thr	Ile	Ser	Met	Gly	Pro	Cys	Ala	Arg	Gly	Ser	Pro	Met	Asn	Ser	Ser				
			40					45					50						

Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
55 60 65
Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu Leu Gly
70 75 80
Arg Gln Leu
85

<210> 499
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<220>
<221> UNSURE
<222> 75
<223> Xaa = any one of the twenty amino acids

<400> 499
Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
-10 -5 1
Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
5 10 15
Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
20 25 30 35
Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
40 45 50
Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
55 60 65
Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu Leu Gly
70 75 80
Arg Gln Leu
85

<210> 500
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25...-1

<400> 500
Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
-25 -20 -15 -10
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
-5 1 5
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
10 15 20
Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
25 30 35
Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
40 45 50 55

Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
60 65 70
Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
75 80

<210> 501
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<220>
<221> UNSURE
<222> 101,110,114,136
<223> Xaa = any one of the twenty amino acids

<400> 501
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15 -10 -5 1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15
Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
20 25 30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
35 40 45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Gly Asn
50 55 60 65
Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu Leu Leu Gln Ser Cys
70 75 80
Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met Ile Ile Asp Asn Arg
85 90 95
Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp Thr Xaa His Val Ala
100 105 110
Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly Ile Asn Leu Val Val
115 120 125
Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser Asn His Ile Ala Leu
130 135 140 145
Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile Cys Lys Pro Cys Gly
150 155 160
Thr Gly Gln Asp Phe Lys Glu
165

<210> 502
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<220>
<221> UNSURE
<222> 20,75,82

<223> Xaa = any one of the twenty amino acids

<400> 502

Met	Glu	Ala	Met	Trp	Leu	Leu	Cys	Val	Ala	Leu	Ala	Val	Leu	Ala	Trp
-15					-10					-5					1
Gly	Phe	Leu	Trp	Val	Trp	Asp	Ser	Ser	Glu	Arg	Met	Lys	Ser	Arg	Glu
		5					10					15			
Gln	Gly	Xaa	Arg	Leu	Gly	Ala	Glu	Ser	Arg	Thr	Leu	Leu	Val	Ile	Ala
		20					25					30			
His	Pro	Asp	Asp	Glu	Ala	Met	Phe	Phe	Ala	Pro	Thr	Val	Leu	Gly	Leu
	35					40					45				
Ala	Arg	Leu	Arg	His	Trp	Val	Tyr	Leu	Leu	Cys	Phe	Ser	Ala	Val	Phe
50					55					60					65
Arg	Arg	Glu	Leu	Ser	Glu	Tyr	Thr	Glu	Xaa	Leu	Thr	Ser	Glu	Pro	Leu
				70					75					80	

Xaa Ala

<210> 503

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -57...-1

<220>

<221> UNSURE

<222> 23,30,41,62,63,73,86,95,102

<223> Xaa = any one of the twenty amino acids

<400> 503

Met	Asp	Val	Thr	Gly	Asp	Glu	Glu	Glu	Glu	Ile	Lys	Gln	Glu	Ile	Asn
	-55					-50						-45			
Met	Leu	Lys	Lys	Tyr	Ser	His	His	Arg	Asn	Ile	Ala	Thr	Tyr	Tyr	Gly
	-40					-35					-30				
Ala	Phe	Ile	Lys	Lys	Asn	Pro	Pro	Gly	Met	Asp	Asp	Gln	Leu	Trp	Leu
-25					-20					-15					-10
Val	Met	Glu	Phe	Cys	Gly	Ala	Gly	Ser	Val	Thr	Asp	Leu	Ile	Lys	Asn
			-5					1				5			
Thr	Lys	Gly	Asn	Thr	Leu	Lys	Glu	Glu	Trp	Ile	Ala	Tyr	Ile	Cys	Xaa
	10					15					20				
Glu	Ile	Leu	Arg	Gly	Leu	Xaa	His	Leu	His	Gln	His	Lys	Val	Ile	His
	25					30				35					
Arg	Xaa	Ile	Lys	Gly	Gln	Asn	Val	Leu	Leu	Thr	Glu	Asn	Ala	Glu	Val
40					45					50					55
Lys	Leu	Val	Asp	Phe	Gly	Xaa	Xaa	Ala	Gln	Leu	Asp	Arg	Thr	Val	Gly
			60					65					70		
Arg	Xaa	Asn	Thr	Phe	Ile	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Xaa	Val
		75					80					85			
Ile	Ala	Cys	Asp	Glu	Asn	Pro	Xaa	Ala	Thr	Tyr	Asp	Phe	Lys	Xaa	Asp
	90					95					100				
Leu	Trp	Ser	Leu	Gly	Ile	Thr	Ala	Ile	Glu	Met	Ala	Glu	Gly	Leu	Pro
	105					110					115				
Leu	Ser	Val	Thr	Cys	Thr	Pro									
120					125										

<210> 504
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<220>
 <221> UNSURE
 <222> 83
 <223> Xaa = any one of the twenty amino acids

<400> 504
 Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
 Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
 Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
 20 25 30
 Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
 35 40 45 50
 Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
 55 60 65
 Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
 70 75 80
 Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu
 85 90 95
 Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys
 100 105 110
 Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr
 115 120 125

<210> 505
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<220>
 <221> UNSURE
 <222> 6,14
 <223> Xaa = any one of the twenty amino acids

<400> 505
 Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg Leu His
 -10 -5 1
 Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser Arg Asn
 5 10 15
 Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser Gln Thr
 20 25 30
 Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
 35 40 45

<210> 506
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<220>
 <221> UNSURE
 <222> 41,42,60,64
 <223> Xaa = any one of the twenty amino acids

<400> 506
 Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg
 -35 -30 -25
 Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Asn Leu Leu Ile
 -20 -15 -10 -5
 Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg
 1 5 10
 Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys
 15 20 25
 Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Xaa Xaa Leu Gly
 30 35 40
 Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn Xaa
 45 50 55 60
 Ala Ala Ser Xaa Gln
 65

<210> 507
 <211> 341
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55..-1

<400> 507
 Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu
 -55 -50 -45 -40
 Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His Leu Cys
 -35 -30 -25
 Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala Ala Leu
 -20 -15 -10
 Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val Asp Val
 -5 1 5
 Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys Gln Arg
 10 15 20 25
 Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met Pro Asn
 30 35 40
 Pro Gln Leu Asn Ile Lys Ala Leu Phe Gly Leu Phe Ser Arg Lys
 45 50 55
 Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln Gly Asp
 60 65 70

Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn Val Phe
 75 80 85
 Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys His Ser
 90 95 100 105
 Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala Arg Lys
 110 115 120
 Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys Glu Pro
 125 130 135
 Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala Leu Asn
 140 145 150
 Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys Pro Gly
 155 160 165
 Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe Ile Trp
 170 175 180 185
 Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala Asn Ala
 190 195 200
 Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp Leu Phe
 205 210 215
 His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu Ser Ala
 220 225 230
 Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met Asp Leu
 235 240 245
 Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu Leu Glu
 250 255 260 265
 Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala Arg Leu
 270 275 280
 Ser Gly Ser Cys Leu
 285

<210> 508
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<220>
 <221> UNSURE
 <222> 9,32,37,50,51,55
 <223> Xaa = any one of the twenty amino acids

<400> 508
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Ile Ile
 -10 -5 1 5
 Leu Gln Xaa Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Xaa Tyr Leu Lys Ile Xaa Lys
 25 30 35
 Gly Asp Gly Gly Ser Gly Ser Lys Gly Arg Pro Xaa Xaa Gln Thr Glu
 40 45 50
 Xaa Phe Leu Cys Ile Ser Lys Pro Ser Ser Phe Leu

55

60

65

<210> 509

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 509

Met	Glu	Glu	Ile	Ser	Ser	Pro	Leu	Val	Glu	Phe	Val	Lys	Val	Leu	Cys
-25						-20					-15				
Thr	Asn	Gln	Val	Leu	Ile	Thr	Ala	Arg	Ala	Val	Pro	Thr	Lys	Lys	Ala
-10					-5					1				5	
Ser	Val	Arg	Cys	Val	Glu	Lys	Arg	Phe	Trp	Ile	Pro	Lys	Thr	Thr	Ser
		10					15					20			
Lys	His	Leu	Ser	Arg	Cys	Ile	Asp	Gly	Ile	Ser	Gly	Phe	Leu	Asn	Asp
	25						30				35				
Phe	Thr	Phe	Cys	Leu	Glu	Phe	Ser	Arg	His	Arg	Cys	Gln	Leu	Thr	Glu
40						45					50				

<210> 510

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -44...-1

<400> 510

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys	Ile
			-40					-35					-30		
Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala	Gly	Ile
		-25					-20					-15			
Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	Val	Val	Tyr
	-10					-5					1				
Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	Cys	Gly	Val	Phe
5				10				15						20	
Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	Ser	Asn	Ala	Gln	Val
		25						30				35			
Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	Gly	Arg	Thr	Gly	Ala	Arg
	40						45				50				
Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	Met	Phe	Gly	Ser	Leu	Ile	Ala
	55					60				65					
Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val
	70				75					80					
Tyr	Pro	Gly	Leu	Ala	Val	Phe	Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser
85				90				95							100
Thr	Leu	Ile	Tyr	Lys	Phe	Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr		
				105				110							

<210> 511

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 511

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Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
      -25                      -20                      -15
Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
      -10                      -5                      1
Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
5                      10                      15                      20
Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
      25                      30                      35
Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
      40                      45                      50
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
      55                      60                      65
Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
      70                      75                      80
Thr Asp Thr Gly Ser His Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly
85                      90                      95                      100
Ile Trp
```

<210> 512

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -62...-1

<220>

<221> UNSURE

<222> -46,125

<223> Xaa = any one of the twenty amino acids

<400> 512

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Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg
      -60                      -55                      -50
Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys
      -45                      -40                      -35
Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val
-30                      -25                      -20                      -15
Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
      -10                      -5                      1
Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu
      5                      10                      15
Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro
      20                      25                      30
Val Gln Ser Asn Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys
35                      40                      45                      50
Thr Ile Gly Asn Asn Gly Asn Gln Ser His Lys Met Thr Thr Ser Arg
      55                      60                      65
Cys Val Arg Leu Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val
```

			70					75					80				
Trp	Ile	Ser	Glu	Gln	Pro	Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr		
		85					90					95					
Met	Pro	Thr	Trp	Ala	Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg		
	100					105					110						
Ile	Glu	Asn	Phe	Lys	Ser	Gly	Val	Asp	Ala	Xaa	Ser	Ser	Tyr	Phe	Lys		
115					120					125					130		
Ile	Phe	Lys	Thr	Lys	His	Asp											
				135													

<210> 513
 <211> 180
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<220>
 <221> UNSURE
 <222> 4,78,112
 <223> Xaa = any one of the twenty amino acids

<400> 513																	
Met	Asn	Thr	Val	Leu	Ser	Arg	Ala	Asn	Ser	Leu	Phe	Ala	Phe	Ser	Leu		
-25					-20				-15						-10		
Ser	Val	Met	Ala	Ala	Leu	Thr	Phe	Gly	Cys	Phe	Ile	Xaa	Thr	Ala	Phe		
			-5					1				5					
Lys	Asp	Arg	Ser	Val	Pro	Val	Arg	Leu	His	Val	Ser	Arg	Ile	Met	Leu		
	10					15					20						
Lys	Asn	Val	Glu	Asp	Phe	Thr	Gly	Pro	Arg	Glu	Arg	Ser	Asp	Leu	Gly		
	25				30					35							
Phe	Ile	Thr	Phe	Asp	Ile	Thr	Ala	Asp	Leu	Glu	Asn	Ile	Phe	Asp	Trp		
40					45				50					55			
Asn	Val	Lys	Gln	Leu	Phe	Leu	Tyr	Leu	Ser	Ala	Glu	Tyr	Ser	Thr	Lys		
			60					65						70			
Asn	Asn	Ala	Leu	Asn	Gln	Xaa	Val	Leu	Trp	Asp	Lys	Ile	Val	Leu	Arg		
			75				80						85				
Gly	Asp	Asn	Pro	Lys	Leu	Leu	Leu	Lys	Asp	Met	Lys	Thr	Lys	Tyr	Phe		
	90					95						100					
Phe	Phe	Asp	Asp	Gly	Asn	Gly	Leu	Xaa	Gly	Asn	Arg	Asn	Val	Thr	Leu		
	105				110					115							
Thr	Leu	Ser	Trp	Asn	Val	Val	Pro	Asn	Ala	Gly	Ile	Leu	Pro	Leu	Val		
120					125					130					135		
Thr	Gly	Ser	Gly	His	Val	Ser	Val	Pro	Phe	Pro	Asp	Thr	Tyr	Glu	Ile		
				140					145					150			
Thr	Lys	Ser	Tyr														
			155														

<210> 514
 <211> 120
 <212> PRT
 <213> Bos taurus

<400> 514
 Met Met Thr Gly Arg Gln Gly Arg Ala Thr Phe Gln Phe Leu Pro Asp

1		5		10		15									
Glu	Ala	Arg	Ser	Leu	Pro	Pro	Pro	Lys	Leu	Thr	Asp	Pro	Arg	Leu	Ala
		20						25					30		
Phe	Val	Gly	Phe	Leu	Gly	Tyr	Cys	Ser	Gly	Leu	Ile	Asp	Asn	Ala	Ile
		35					40					45			
Arg	Arg	Arg	Pro	Val	Leu	Leu	Ala	Gly	Leu	His	Arg	Gln	Leu	Leu	Tyr
		50				55					60				
Ile	Thr	Ser	Phe	Val	Phe	Val	Gly	Tyr	Tyr	Leu	Leu	Lys	Arg	Gln	Asp
65					70					75				80	
Tyr	Met	Tyr	Ala	Val	Arg	Asp	His	Asp	Met	Phe	Ser	Tyr	Ile	Lys	Ser
			85					90					95		
His	Pro	Glu	Asp	Phe	Pro	Glu	Lys	Asp	Lys	Lys	Thr	Tyr	Gly	Glu	Val
		100						105					110		
Phe	Glu	Glu	Phe	His	Pro	Val	Arg								
		115					120								

<210> 515
 <211> 1082
 <212> DNA
 <213> Homo sapiens

<400> 515

gatccagac	ctcggcttgc	agtagtggtta	gactgaagat	aaagtaagtg	ctgtttgggc	60
taacaggatc	tcctcttgca	gtctgcagcc	caggacgctg	attccagcag	cgccttaccg	120
cgcagcccga	agattcacta	tggtgaaaat	cgccttcaat	accctaccg	ccgtgcaaaa	180
ggaggaggcg	cggcaagacg	tggaggccct	cctgagccgc	acggtcagaa	ctcagatact	240
gaccggcaag	gagctccgag	ttgccaccca	ggaaaaagag	ggctcctctg	ggagatgtat	300
gcttactctc	ttaggccttt	cattcatctt	ggcaggactt	attgttggtg	gagcctgcat	360
ttacaagtac	ttcatgccca	agagcaccat	ttaccgtgga	gagatgtgct	tttttgattc	420
tgaggatcct	gcaaattccc	ttcgtggagg	agagcctaac	ttcctgcctg	tgactgagga	480
ggctgacatt	cgtgaggatg	acaacattgc	aatcattgat	gtgcctgtcc	ccagtttctc	540
tgatagtgac	cctgcagcaa	ttattcatga	ctttgaaaag	ggaatgactg	cttacctgga	600
cttggttgctg	gggaactgct	atctgatgcc	cctcaatact	tctattgtta	tgccctccaaa	660
aaatctggta	gagctctttg	gcaaactggc	gagtggcaga	tatctgcctc	aaacttatgt	720
ggttcgagaa	gacctagtgt	ctgtggagga	aattcgtgat	gttagtaacc	ttggcatctt	780
tattttacca	ctttgcaata	acagaaaagtc	cttcgcgctt	cgtcgcagag	acctcttgct	840
gggtttcaac	aaacgtgccca	ttgataaatg	ctggaagatt	agacacttcc	ccaacgaatt	900
tattgttgag	accaagatct	gtcaagagta	agaggcaaca	gatagagtgt	ccttggtaat	960
aagaagtcag	agattttacaa	tatgacttta	acattaaggt	ttatgggata	ctcaagatat	1020
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aa						1082

<210> 516
 <211> 559
 <212> DNA
 <213> Homo sapiens

<400> 516

ctgctccagc	gctgacgccg	agccatggcg	gacgaggagc	ttgaggcgct	gaggagacag	60
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aagcacaggg	aagcagaaat	gagaaacagt	atcttagccc	aagttctgga	tcagtcggcc	180
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559

<210> 517

<211> 110

<212> PRT

<213> Homo sapiens

<400> 517

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<210> 518

<211> 4544

<212> DNA

<213> Homo sapiens .

<400> 518

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<211> 1779

<212> DNA

<213> Mus musculus

<400> 519

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